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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: gb_ba:*
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375
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE	SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 AX036541 LOCUS		C 45	c 43		40	c. (38)		C 34		c 31		228	c 26 27		221	c 21		18		c 15		12	10	ယ ထ	7		C A 3	21	Result No.
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Hirudinidae; Hirudo. matter, W., Hofmann, U., Fotev, Z. sesion			DNA linear PAT 16-NOV-2000		035475 Plasmodi	2659 Mus mus	1380 Strongy 4634 Homo sa	3702 Plasmod	. ~ :	3749 Homo sa 3032 Arabido	attus	ss omc	r7 end	nio r	lasmoc	lasmoc us mus	on (2	ĕ	lasmod Smo sa	omo sa	omo sap	norhabd	rosophi	ictyost	AFZ169/3 DIOSOPHII AC014497 Drosophil	ius mus	equenc omo sa	eduence	enor	menorha	nce	Description

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KEYWORDS
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Best Local :
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                                               Direct Submission
Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 189967)
                                                                                                                                                                                                                                                                                                       AL833802 189967 bp DNA
Mus musculus chromosome 4 clone RP23-17A4,
PROGRESS ***, 13 unordered pieces.
Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1.
                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                       AL833802.3 GI:21911787
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(DE); GUESSOW DETLEF (DE)
Location/Qualifiers
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                                 Jul 19, 2002 this sequence version replaced gi:21738804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAC16481.1"
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Pred. No. 6.6e-86;
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Insert size: 215919; 10.9% error; agarose-fp
Quality coverage: 5.28x in Q20 bases; sum-of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator: 100% of reads
Consensus quality: 186623 bases at least Q40
Consensus quality: 187480 bases at least Q30
Consensus quality: 188086 bases at least Q20
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Contact: humquery@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coverage: 4.68x in Q20 bases; agarose-fp
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146368 151984; contig of 5617 bp
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152085 184112: cont
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184213 189967: contig of 5755
Location/Qualifiers
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8455 8554: gap of 100 bp
8555 19307: contig of 10753 bp in length
19308 19407: gap of 100 bp
19408 27097: contig of 7690 bp in length
27098 27197: gap of 100 bp
27198 40822: contig of 13655 bp in length
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                                                                              /note="assembly_fragment:01468
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus
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    Summary Statistics

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contig of 32028 bp in length
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5755 bp in length
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RESULT 3
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                                                                                              Direct Submission
Submitted (22-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
       Center:
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                   23, 2002 this sequence version replaced gi:21690116
Wellcome Trust Sanger Institute
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fragment_chain:3"
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fragment_chain:3"
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fragment_chain:3
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
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48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 AACAGAAAATATACAGACTTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                               GATTAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 204885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGAC 276
                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
1 (bases 1 to 40090)
                                                                                                       Caenorhabditis elegans.
                                                                                                                                             HTG
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                                                                                                                                                                                                                          Caenorhabditis elegans
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                                                                                                                                                                    AC006611.1 GI:4263327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-207H16 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VECTOR: pBACe3.6.
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/clone_lib="RPCI-23"
37887 c 37484 g 67430 t
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                            cosmid
                                                                                                                                                                                                                                                 40090 bp
                                                                                                                                                                                                                       C30F8, complete sequence.
                                                                                                                                                                                                                                                    DNA
                          Caenorhabditis
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200 bp overlap. Actual start of this cosmid is at base position 197 of C30F8; actual end is at 40090 of C30F8.

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REFERENCE
AUTHORS
TITLE
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  The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-FEB-1999) Genome Sequencing Center, Washington
Submitted (23-FEB-1999) Genome Sequencing Center, Washington
Submitted (23-FEB-1999) Genome Sequencing Center, Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-FEB-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA 8 (bases 1 to 40090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Latreil, P., Twyman, B. and Wilson, R. The sequence of C. elegans cosmid C30F8
                                                                                                                                                                                                                 or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-OCT-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.H.
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                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemist:
                                                                                                                                                                                                                                                                                                                                                                   neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-APR-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                               For a graphical representation of this cosmid sequence and its
                                                                                                                                                                                               more than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis,
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                                                                                               {www.wormbase.org/db/seq/sequence?name=C30F8; class=Sequence}
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Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
     cosmid is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63110, USA
                                                    NEIGHBORING COSMID INFORMATION
  8300 bp
overlap; the 3'
                                                                                                                                                                                                                                                                                             an alternate chemistry
     cosmid is Y110A7A,
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source

Location/Qualifiers

/organism="Caenorhabditis elegans" /strain="Bristol N2" /db_xref="taxon:6239"

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORReome cloning project (http://worfdb.dfcl.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans researchers truns are predicted using the program trunscans GenBank submissions, are predicted using the program trunscans (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

gene CDS CDS misc_feature misc_feature complement(21528. .21529)
/note="SI1 trans-splice site; see yk821a09.3"
complement(21534. .21535) /note="coded for by the following C. elegans cDNAs: yR710g2.3, yk449d2.3, yk705g11.3, yk745d7.3, yk165b6.3, yk809d10.3, yk807a04.3, yk702g3.3, yk105b9.5, yk169b6.5, yk306e11.3, yk306e11.5, yk431f1.3, yk431f1.5, yk449d2.5, yk479e6.5, yk859d05.5, yk710g2.5, yk702g3.5, yk449d2.5, yk479e6.5, yk753e04.5, yk821a09.5, yk809d10.5, yk809d10.5, yk773c05.5, yk705g11.5, yk754e11.5, yk807a04.5, yk809d10.5, yk754e11.3, yk808h07.3, yk888h07.3, yk888 Join (25607. .25684,27245. .27344,27393. .27492,27665. .2 28346. .28436,28489. .28707,28818. .29897,29946. .30020, 30070. .30315,32038. .32325,32760. .32891) //gene="C30F8.4" complement(19565. .21512) /gene="C30F8.2" /translation="MGEFLFNIDHGYLEAL/RGLKGGLLAQADYANLYQCETLEDLKL HIQSTDYGNFLANEPGAITVQVIDEKLEKTVEETHLRNNALEPLAFFLDYITYSYM IDNIILLITGTLHQREISELLINKCHPUGSFEOMEAIHLASTPAELYNAVLVDFPLANY FVDCINEQDLDEMNVEVIRNTLYKAYIEDFYKFCAGLGGKTAEVMCDILAFFADRRSI complement(join(19565. .19654,20030. .20101,20153. .20407, 20460. .20617,20879. .21057,21102. .21273,21392. .21512)) IITINSFDTELSKDDRQKLYPRCGKLFPDGLTGLSRADDYDQVKQVCEFYSDYKPLFE GSGNGPGEKTLEDKFFEHEVKLNVHSYLHQFHFGVFYAFIKLKEQEMRNIIWIAECIS /product="Hypothetical protein C30F8.2"
/protein_id="AAK85455.2"
/db_xref="GI:16259229" /codon_start=1 /product="Hypothetical protein C30F8.4a" /protein_id="AAKB8457.1" /db_xref="G1:15150650" yk739d9.5, yk284c11.3, yk649h5.5" QRHRTKIDNYIPIM" /codon_start=1 /gene="C30F8.2" [www.wormbase.org/db/seq/sequence?name=C30F8.2;class=Seque /note="for a graphical representation of this gene see: /clone="C30F8" /chromosome="I" /note="similar to protein kinases (PFam; pkinase, score; 183.25); coded for by the following C. elegans cDNAs: yk739d9.5, yk284c11.3, yk284c11.5, yk465a7.5, yk739d9.3, /gene="C30F8.4" note="SL1 trans-splice site; see yk809d10.5" www.wormbase.org/db/seq/sequence?name=C30F8.4a;class=Sequ note="for a graphical representation of this gene see: 3289

.27859

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RESULT 5
AC006845
                                  ACCESSION
                                                                                            DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  187 TACATCGTTTTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 GAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAATCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TATTICTIGATITCCTTCCTTTGCCTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAA 66
                                                                                                                                                                                                                                                                       AAAAAATTTTTT 8714
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGC
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AC006845
AC006845.1 GI:4263503
                                                       5 unordered pieces.
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/gene="C30F8.3"
/note="for a graphical representation of this gene see:
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IMHIEQGSRPPCPEKCPTALINFIRSKMWAIEPHKRPTVDQIYAIIEDVRQQIIQNIP
PEQIIVGKPWTAAGVIVAEMSSLPGLTLYRTWEDQKRQAEEDAKWLEQEDDEDEDDQD
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GELREVLQQEKDWLPLRILTLECSQICDSLYVLHSTRFVHRDIAARNILVCSPQCVKL
ADFGLSRALDYDAVYTASRGKLPIKWLAPESVWYRQFSMASDVMMFGVCMWELFSLGV
KPWAGVTNSDVIMHIEQGSRPPCPEKCPTALY BIRSKMWAIEPHKRPTVDQIYAIIE
DVRQQIIQNIPPEQIIVGKPWTAAGVIVAEMSSLPGLTLXRTWEDQKKRPEDAKWLE
QEDDEDEDDQDIDQIPSTSHSSVENIRTSNGYLHHTPTSTRSLRFEDKTSRGLRRSVD
GVCDAVTKLONSFNNLTHNDDFLHSVKEVTSQLREMLIVASGMRDRVTTTTQRTDVDM
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ADHHLEDLDIEACIQSLIWLHNPGERHSHLKTFTAYIKESATSPESIIRSLAL
LLEVVKFDVELFKASLGAGWTKPVELVVGPTFGLSYRLNEFCDSSRLLERTIAEITI
RKMENGSEKTLMQLNLSGAAKFVLITLSTEELSQSLAHLLDGYQMLYNQRDSVEKLKG
IERCEFLTMHEATIRVENNIDSNIRLRRELITLKELIGGGQFGNVYKAVYHDLEKD
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ATIRPKTPNNIDSNIRLERRELITLKELIGGGQFGNVYKAVYHDLEKDERIAVAVKVCK
TDAEPADTQLILQESSLMRNFRHSNIIQLIGVCVDQPMWLVLELAPKGELREYLQQEK
DWLFLRILTLFCSQICDSLYYLHSTRFVHRDIAARNILVCSPQCVKLADFGLSRALDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vtranslation="MLRITQLPHIYARHLPIGVCDEIKLEMRWRFMPQSVYELQATDS
SAFVTLHEQVVDEFFSHVAWRSSVEVALEVAALKVCROPAEHGHRGADHHLEDLDIE
ACIQSLIPNYLHNPGFKHSHLKKTFTAYIKKESATSPNESIIRSLALLLEVVKEDVEL
FKASLGAGWTKPVELVVGPHTGLSYRLNERCDSSRLLELRTIAEITIRKMENGSEKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDQIPSTSHSSVENIRTSNGYLHHTPTSTRSLRFEDKTSRGLRRSVDGVCDAVTKLQN
SFNNLTHNDDFLHSVKEVTSQLREMLIVASGMRDRVTTTTQRTDVDMTKTLIANDMKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="coded for by the following C. elegans cDNAs yk1020h08.5"
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28818. .29897,29946. .30020,30070. .30315,32038. .32325
32760. .32891)
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HFALRLVTGPSPQTAGSGDSLWLHPMLRITQLPHIYARHLPIGVCDEIKLEMRMRFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSRVMGKLQVNGHQATYNTLRRDVVRICGELAVNCTTLQLQLTQPPLENEFSSLLSNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Hypothetical protein C30F8.4b"
/protein_id="AAM15554.1"
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Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum chromosome 2 map 5179259-5183715 strain AX4, *** SEQUENCING IN PROGRESS *** in control of the control
                                              Eukaryota; Mycetozoa;
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Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as
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(bases 1 to 4458)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1
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/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GenelD may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K., Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                   Sequence 5 from Patent WO9950284.
AX015902
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            PATENT: WO 9950284-A 5 07-OCT-1999;
AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP
ANDREAS (DE); WIRTH THOMAS (DE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Noegel, A.A.
                                                                        development
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Aigner, T., Hess, J., R
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                Nucleic acid molecules which code
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Location/Qualifiers
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NOTE: This is a 'working draft' sequence.
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Sequence 11 from Patent WO9950284.
AX015908
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11814 c 10825 g 14150 t
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11787 c 10868 g 14209
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Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jul 10, 2002 this segmence "Corres"
                                                                                                                                                                                                                                                                                 AF312994 228283 bp DNA linear ROD Mus musculus chromosome 1 clone MML, complete sequence. AF312994
      Submitted
                    Rump,A., Hess,J., Galgoczy,P., Wirth,T. and Rosenthal,A. Direct Submission
                                                                                                  1 (bases 1 to 228283)
Rump,A., Hess,J., Galgoczy,P., Wirth,T. and Rosenthal,A.
Genomic sequence from mouse chr. 1
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                      Mus musculus
                                                                               Unpublished
                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                              AF312994.1 GI:18182288
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2 (Dases 1 to 119191)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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(12-OCT-2000) Genome Analysis,
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26845 c 25557 g
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53.7%;
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Pred. No. 0.34;
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Institute of Molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-DEC-1999) Department of Biochemistry, University, Beckman Center, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
Drosophila melanogaster
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Drosophila melanogaster 1(2)01289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 20796)
Manning,G., Micklem,D.R. and Krasnow,M.A.
Sequence of 1(2)01289 genomic locus
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AF216973
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                                                                                                                                                             join(<865. 1470,3154. .3310,3382. .3548,3980. .4015, 6598. .6780,6911. .7054,7117. .7250,7315. .7495,7567. .981, 8252. .8566,8627. .9271,9325. .9570,9575. .7958,79576. .9958, 15122. .1523,15483. .15806,15871. .16059,16118. .16255, 17488. .17670,17723. .17854,18603. .18799,18817. .18983, 19047. .19203,19257. .19423,19484. .19666,19733. .20489)
                                                                              /product="1(2)01289 long form"
join(<1153. .1470,3154. .3310,3382. .3548,8252. .8566,
8627. .9271,9325. .9507,9575. .9712,9776. .9958,10019.
                                                                                                                                                                                                                                                                                                                  <865. .20489
/product="1(2)01289 H9 form"
join(1257. .1470,3154. .3310,3382. .3548,3980. .4015,
                                          12437. .12919,13190. .14706)
/gene="1(2)01289"
                                                                                                                                              /gene="1(2)01289"
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                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster
/db_xref="taxon:7227"
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/db_xref="taxon:10090"
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Pred. No. 0.35;
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Query Match
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                                                                                                                        Conservative
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KLAHEIGIFAFPALVYYETGVPIMYDGNIASNQDVFNWILEQKADQSIQLINROQLFE
YIGTKDFLAVFYYKEDDDSBRVLHHELIDDEAAEXGIYIVKHHDKLMAKKYGFNU
PGLTYFRKGKYINYDGDIDDEEVLDWLTSPANMEMTDHIEQVNRKMFEKIRKNSDYV
AVIFYSDECKQCFRVLAEVEHIDDEADKAGIDFVKIDDEADKAGYOFSHDVFYALPAIVFFKP
TSKBETKYGADALYEEBGILTWHLTGKOPSGYVIEDLEGERLVHLIEESGSIAVVFYAD
GCEQCTKVLEELENIDDDCDKHGITFFVKTRDFSVADGYGVHEXPALYYFEGGIPNVFE
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RILNELENIDDELEKEGIVIVRIDNAAEAKEYGLDHLPALIYFENKIPALYEGDLMNE
DEVLEWLLVQKKTATIEEVTDEILVTLINEHEYVVVFFTGPCEFGETCEHTLNALESI
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VPKLIYFEKGIPTIYEGNLEDEEKLLKWLTDQTSSDQIEDITDEMLDLIIEKMPHVAV
LFYDKDQKKSQKILAELENIDDECDQNDIAFVKIDDDKBAKEWGIDEIPSIVLFERGI
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GFVK.HDEALADEYNIGNLPALVYYRIGOTPIIYEGELOREEDVLEWLVQNKSTGDEDD
VIEDVTSKTLSTLISNIGNLLVYLFUHGNDDSMTVLEELEGIDDDCDKHEGIGFVKIDD
AKAAADYGIDSIPAIVYFEKEIPNVYDGDLMDEEQILKWLLGQLERDEIEDVTDEMLD
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YFENKIPALYEGDLMNEDEVLEWLLVQKKTATIEEVTDEILVTLINEHEYVVVFFTGP
CEPGETCEHTLNALESIDDELDEAGIIFVTTEDTGIAKKYNVKTYPRLVFFRNRDPLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YALIALAVAFVYYTAFLLQCFKPAPPPPVQHPKQS"

JOIN(1257. 1470,3154. 3310,3382. 3548,8252. 8566,

1011(1257. 9257. 9507,9575. 9712,9776. 9958,10019. 10069,

12437. 12919,13190. 13227)
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EIKNEIEEVNRKMLDKLLEENEFLAVFFYEHNQPDSTAALEKLENIDSETDNLDITFV
KMADSRYAKKWGVTKLPAMVYFRRRFPSIYRGDLLSEDEVLEWLRKNRFRQPELNIFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDELDEAGIIFVTTEDTGIAKKYNVKTYPRLVFFRNRDPLHFTGDLDDEDEVLAWITD
DETLEIPGKIEEVNVKMLDKILAENDHVVVFFYAEGDKKAQKILNELENIDDECEEKD
IDFVKTSDDDIDKEYDLPGLPALAFYRHKFRTIYTGDLMKEEEILEWVIDLHESTADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6598. .6780,6911. .7054,7117. .7250,7315. .7495,7567. .7881, 8252. .8566,8627. .9271,9325. .9507,9575. .9712,9776. .9988, 15122. .15253,15483. .1566,15871. .16059,16118. .16255, 17488. .17670,17723. .17854,18603. .18759,18817. .18983, 19047. .19203,19257. .19423,19484. .19666,19733. .19920)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKNDECFYVGLGHDGHSAKRGNNFVPNDYKPFQCCPTKLEKSTKVPKMTAQRIGHSEG
DQGKRPSGGNFQFASQASSKSSTKPAAIKKQAKPSKDTDDDDEDDEDKPLVKVSYANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDKRLAKQYGIKNFPALTYFREKEPIIYDGDLMDEEGVLDFLTSLEAMDLPDRIEEV
NAKILQKIIEDTDFVAVLFYDKDQKKSQKILAELENIDDECDQNDIAFVKIDDDKEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEAVIEEVNAKQLEKLLADKDYVAVFWYARSCVTCDKVLAELEKIDDDTDSFGVDFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="1(2)01289 H9 form"
/protein_id="AAF34747.1"
/db_xref="GI:6984066"
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LELIDDECDVFGIHMVKIQDPQLAKRYSIKTFPALVYFRNGNPLLFEGDLQNEQSVLE
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/protein_id="AAF34746.1"
/db_xref="GI:6984065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDDTDKHGIQFVKSNDVKLAHEIGIFAFPALVYYETGVPIMYDGNLKNENRVLQWLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KILNELENIDDECEEKDIDFVKTSDDDIDKEYDLPGLPALAFYRHKFRTIYTGDLMKE
EEILEWVIDLHESTADVIESVDRKTLQVLINDVEHLAVFFYDDECESCSDILEELENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTGDLDDEDEVLAWITDDETLEIPGKIEEVNVKMLDKILAENDHVVVFFYAEGDKKAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EWGIDEIPSIVLFERGIPHIYEGDLMKEDELLGWLVHQKRYSEIPEVTDEMKDKLVEN
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/gene="1(2)01289"
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                                                                                                                                                                                                                                                                                                                                                                                                                    rSGGSNKPQAGKKPVGKGQDNDDQSQEVEKVSKQKSAKKSGKLNVKSGYLSVGVRQQF
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                                                                                                                                                          12.1%;
49.6%;
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                                                                                                                                                               Score 45.2; DB 3; Pred. No. 0.45;
                                                                                                                            Mismatches 118;
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SOURCE
ORGANISM
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AC014497
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                                                 DEFINITION
                                                                                           AC116976/c
                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
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  ACCESSION
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70828 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACAAGGACGAGGATAACGA 70887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10850 AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 10903
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                                                                                                                                                                                          71008
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                                                                                                                                                                                                                                                                                                                                    261 AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                              201 AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA 260
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                                                                                                                                                                                          AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 71061
                                                                                                                                                                                                                                    TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGATTA 374
                                                                                                                                                                                                                                                                                     CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA 71007
                                                                                                                                                                                                                                                                                                                                                                                 AGAAGATAATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA 70947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 87767)
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AC014497
AC116976 132000 bp DNA linear HTG 05-APR-20 Dictyostelium discoideum chromosome 2 map 2066573-2198571 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces. AC116976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rockville, MD, USA
This sequence was identified as CDM:10210380 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACO14497 B7767 bp DNA linear HTG 16-NOV-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or further information on this sequence e-mail to fly@celera.com NOTE: This is a 'working draft' sequence. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
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/db_xref="taxon:7227"
19624 c 19272 g 23855 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45.2; DB 2; Length 87767; Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the submitter.
                                                                            HTG 05-APR-2002
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                                                                                                                                                                                                                                                                                                                          Db 124082 ATGAAGATGAAGAATTTAATGAAGATGAAGATGAAGAA 124045
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ORIGIN
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Best Local Similarity
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JOURNAL
                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                       338 GTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 AAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110;
                                          Drosophila melanogaster
                                                                                       HTG; HTGS_PHASE1.
                                                                                                                                                                     AC007624 167062 bp DNA Drosophila melanogaster chromosome 2 cl. 10.F.15 map 42E-43A strain y; cn bw sp,
                                                                                                                                                                                                                    AC007624
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Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 132000)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
Noegel,A.A.
                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                            Drosophila melanogaster.
                                                                                                        AC007624.5 GI:6563437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum. Dictyostelium discoideum
  Neoptera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Funding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence and Analysis of Chromosome 2 of Dictyostelium
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                                                                                                                                                   unordered pieces.
Endopterygota; Diptera; Brachycera; Muscomorpha;
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/chromosome="2"
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                                                                                                                                                                   wA linear HTG 13-DEC-1999 clone BACR10F15 (D621) RPCI-98 sp, *** SEQUENCTION
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Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Dec 13, 1999 this sequence version replaced gi:5670596.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G. Butenhoff,C., Champe,M., Chavez,C., Chew,M., Classiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacaleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Syirskas,R.R., Man,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 181771)

S Celniker, S. E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibeywam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Nunoo, J.,
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                                                                                                                                                                                                                                                                                Drosophila melanogaster
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
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/strain="y; cn bw_sp"
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165373: gap of o
165599: contig
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2R, region 42D-42E, BAC clone
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.1%;
Best Local Similarity 49.6%;
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                                                                                                                     24283 CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA
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                                                          321 TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTA 374
AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler, Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaverl,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 2R, region 42D-42E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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On Sep 6, 2001 this sequence version replaced gi:13374651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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                                                                                                                                                                                               Score
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAS75452
AAT89346
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AAZ23891
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3873.850 Million cell updates/sec
                                                                                                                                                                                           Description
                  DNA encoding novel
Human p160 cDNA 16
Human p160 cDNA 16
                                                                                                                 Murine LOBO genomi
                                                                           Human ovarian anti
                                                                                                                                                    Platelet binding i
                                                                                             Drosophila melanog
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Arabidopsis thalla DNA encoding novel Listeria monocyte DNA encoding novel Plasmodium falcipa Shrimp white spot Shrimp white spot Human breast cell	AAC47605 AAS90738 ABA03041 ABA03041 AAA70213 AAA62819 AAA62889 AAA6289 AAA6289 AAA6289 AAA6289 AAA6289	21 23 23 24 22 22 22 22 22 22 22 22 22 22 23	1448 1072 2944528 1622 2658 3543 305107 315 315 315 315	10.23 10.23 10.01 10.00 10.00 10.00 9.99 9.99	38. 4 37. 8 37. 6 37. 4 37. 2 37. 2	35 35 35 37 38 39 44 42 42 43
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Human breast cell Human foetal liver Probe #12754 for g Probe #12047 for g Probe #18095 used t Probe #7803 used t Human breast cell Human foetal liver Probe #2825 for ge Probe #28917 used t Probe #2917 used t Probe #2918 used t Probe #2782 used t Probe #2782 used t Sarcoma-a Nucleotide sequenc Kaposi's sarcoma-a KSHV LUR DNA (nucl	ABA49279 ABA67193 ABA67193 ABA67193 ABA122114 AA117409 AA117409 AA117409 AA117812 ABA44123 ABA44123 ABA44575 ABA441231 AA112874 AA112874 AA112874 AA1302901 ABA93487 AAV73805		766 766 766 766 766 1944 1944 1944 1944 1944 1944 3489 3489	11000000000000000000000000000000000000	u u u u u u u u u u u u u u u u u u u	10 11 12 13 14 16 16 17 18 18 19 20 20 21 22 23

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ALIGNMENTS

AAA28180 standard; cDNA; 375 BP

AAA28180;

29-JAN-2001 (first entry)

Platelet binding inhibitor protein Saratin encoding cDNA sequence.

Saratin; medicinal leech; thromboembolic disease; intraocular lens; collagen-dependent platelet adhesion inhibition; posterior capsule opacification; ss.

Hirudo medicinalis.

/*tag= a /product= "Saratin" /note= "Platelet adhesion inhibitor protein" /*tag= Location/Qualifiers

WO200056885-A1

28-SEP-2000.

RESULT 1
AAAA28180
ID AAAA2
XX AAA
AC AAA2
XX Plat
XX Sara
XX Sara
XX Sara
XX Sara
XX Coll
XX FH Key
FH Key
FT CDS
FT CDS
FT CDS
FT XX WO20
XX WO20
XX 10-M
XX 11-M
XX 11-M
PR 118-M
PR 118-M
XX (MER 18-MAR-1999; 12-MAY-1999; 10-MAR-2000; 2000WO-EP02117

99EP-0105530 99EP-0109503

(MERE) MERCK PATENT GMBH

a

ABA9052

Genomic sequence

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cc or antagonists. Saratin is useful for treating thromboembolic processes, cand for manufacturing a medicament for treating thromboembolic diseases. It is useful for preventing thrombotic diseases. Saratin is also useful for coating artificial surfaces, since use of Saratin renders them come use of saratin renders them can ever the streating for coating artificial surfaces, since use of Saratin renders them can ever the streating for coating natural collagen surfaces. Furthermore, Saratin is useful for modifying intraocular lenses in order to lessen the can be contacted for coating natural collagen surfaces. Furthermore, Saratin is continuously of the lens material, for contacting the lens surface, or compose to coasinking to modify the lens material. The lens material coular implants, or covalent crosslinking to modify the lens material. The lens material coular implants, core for covalent crosslinking to modify the lens material. The lens material coular implants, core problems contributed by stimulated cell growth. In combination with other composed coular implants, and the completely overcome posterior capsule opacification. The continuous immunospecific for Saratin, as well as Saratin itself, are useful for measuring samples derived from host cell cultures or from a created subject. The present sequence represents cDNA encoding the content of the country of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding Saratin, an expression vector comprising the DNA sequence, a host cell transformed with the expression vector, antibodies immunospecific for Saratin, and methods for identifying Saratin agonists
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Pred. No. 3.3e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1999
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CAGGTAATGCGGCAGGTACAGGTGACGAGGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                          AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTTGAAGAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116;
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                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine LOBO protein described in the method of the invention.
        ABL06114;
                                                                                                                  9498
                                                                                                                                                                                                                                                                                                         9318
                                ABL06114 standard; cDNA; 15935 BP
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 161-189; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-601320/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1999
                                                                                                                                                                                                                                                                                                                                143 ATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9950284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine LOBO homologue genomic DNA fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ23896 standard; DNA; 49999
                                                                                                               CAGGTAATGCGGCAGGTACAGGTGACGAGGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                          ATTTTGAAGAAAAAAATCTAATATTACAGATTCCAGACTTGTTATATAGAAGAAGAAG
                                                                                                                                                                                                       AATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATG
                                                                                                                                                                                                                                                                     ACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAA 262
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rump A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98DE-1013799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-EP02055
                                                                                                                                                                                                                                                                                                                                                                                 12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hess J,
                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                 Score 45.8; DB Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aigner T,
                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wirth T;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length 49999;
                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The methods
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                        9437
                                                                                                                                                                                                                                                                                                    9377
                                                                                                                                                                                                         322
                                                                                                                                                                                                                                                                                                                                   202
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                                                            RESULT 5
ABQ54916
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                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                            10070
                                                                                                                                                                                                                                                     10190
                                                                                                                                                                                                                                                                                                           10250 TAATGATGGGGACGACGATGACGGAGATGACAATGAGGACGACGACGAGGATAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI0181075) and the encoded proteins (ABLO1840-ABB16175) and the encoded proteins
              ABQ54916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification, at ftp.winc '-'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                          ABQ54916 standard; cDNA; 2438
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15935 BP; 4219 A; 3351 C; 3394 G; 4971 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 12824; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                         321
                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                           141 TGATCTTGACGAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 12824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                AGAAGATAATAATGACGACGAAGATGACGATGAAGACGACGAGGATGACGAAGAAGA
                                                                                                                       AGAAGATAATAATGAAGACGACAAGGACGATGAGGATGAAAACGACGAAGATGA 10017
                                                                                                                                                   TGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGATTA 374
                                                                                                                                                                                     CAATAATGATAACGACGAGGATGACGAAGAAGATAATAATAAGGACGACGAAGATAACGA
                                                                                                                                                                                                                 AAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGA 320
                                                                                                                                                                                                                                                                               AGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGA
                                                                                                                                                                                                                                                                                                                                                                              116;
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB62011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M,
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                           12.1%;
49.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                         Score 45.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                           0.011;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 23;
                                                                                                                                                                                                                                                                                                                                                                            118;
                                                                                                                                                                                                                                                                                                                                                                            Indels
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Length 15935;

WIPO

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Gaps

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Best Local Similarity

52.1%;

Pred. No. 0.009;

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cc encompasses polypeptides 90% identical and polynucleotides 95% identical ct to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen cc polynucleotides, antibodies against human ovarian antigens and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, cc treating, prognosing or preventing various ovary and/or breast-related cd disorders. Such conditions include ovarian cancer and breast cancer, and cd disorders (e.g., infertility, disorders of pregnancy, anovulation, cpolycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine cd disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic cshock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and componitis), immune disorders (e.g., congenital and acquired compondeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, conditatory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and condilate ovarian antigen expression or activity. The polynucleotides may concern the polynucleotides may 
                                                                                                                                                                                                                                        further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The presequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002
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antibody preparation; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian antigen HNBVO53 cDNA, SEQ ID NO:796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 796; 2922pp; English.
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infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
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                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-147878/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP41839
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                                                                                                                                                                                                                                                                                                                  The present
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Query Match

Sequence 2438

BP;

561 A; 761 C; 686 G; 427 T; 3 other;

Score 44.4;

DB 24;

Length 2438;

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RESULT 6
AAS75452
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            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction in recombinant production of (II). The polymerase are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1771 GGAAGAAGAA 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1711
                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #11256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS75452 standard; cDNA; 372
                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 11256; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 CTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGAAGAGGAAGACTTTGAGGAAGAGGAAGAGGATGAAGAGGAATATTTTGAAGA 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGA 305
                                                                                                                                                                                                                                                                                                                                                                                                                             2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEQ INC.
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for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0540217
2000US-0649167
 gene mapping,
disorders or o
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   other
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RESULT 7
AAT89346
ID AAT89346
ID AAT89346
AC AAT8
AC AAT8
AC AAT8
AC Huma
XX P160
KW P160
KW P56-
CS Homo
XX Loal
XX CDNA
PT CDNA
PT Lrea
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PT Lrea
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XX CONA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W.
                    Claim 82; Fig
                                                                                   cDNA encoding p62 and p160 and corresponding proteins - used in the treatment of autoimmune disease and for T and B cell proliferation,
                                                                                                                                                           WPI; 1997-341351/31.
P-PSDB; AAW31186.
                                                                                                                                                                                                                                                                                                                                                                11-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9722255-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human p160 cDNA 160.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 372 BP; 194 A; 27 C; 134 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                        (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                                                                                                    19-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p56-lck; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT89346 standard; cDNA; 3211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GAATGCAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAGACACGGTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATCCCATAAACGGGAGTTCGAGACTCACCTAGGCAACATAGCGAAACCCCATCTGAAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p62; cytoplasmic; T cell; B cell; development; activation;
ation; cellular response; cell proliferation; autoimmune disease;
                                                                   treatment of tumours
                                                                                                                                                                                                                            Shin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                       10;
                                                                                                                                                                                                                                                                                                                    95US-0574959
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/note= "160.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439..3156
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                  175pp; English
                                                                                                                                                                                                                         Strominger JL,
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Pred. No. 0.043;
0; Mismatches 1
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                                                                                                                                                                                                                            Vadlamudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RRESULT 8
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ID AAT66
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XX P166
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XX P17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA sequence encodes a novel p160 (160.2) which is capable of activating transcription of a variety of genes upon activation of p62 and is capable of binding to the p62/p561pk complex to modulate Lck function in a manner similar to p62. The genes transcribed in response to p160 activation likely include those of which are involved in T or B cell development/differentiation, T or B cell activation or production of T or B cell specific factors e.g. lymphokines or antibodies. This p160 polypeptide is also a substrate for serine/threonine kinase activity. p160 polypeptides can modulate degradation of cellular proteins e.g. cell p160 polypeptides can modulate degradation of cellular proteins e.g. cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cycle regulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As p160 boosts B cell response it may be used to treat disorders where this is beneficial, e.g. infections by pathogenic microorganisms, p160 can be used to expand T cell populations for treating infections diseases or cancer and p160 inhibitors could reduce B or T cell responses and may be used to treat a variety of autoimmune diseases, e.g. diabetes mellitus, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p160; p62; cytoplasmic; T cell; B cell; development; activation;
modulation; cellular response; cell proliferation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                               11-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9722255-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT89345 standard; cDNA; 3901 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3211 BP; 649 A; 990 C; 948 G; 624 T; 0 other;
                                                                                                                                                               (DAND ) DANA FARBER CANCER INST INC
                                                                                                                                                                                                                                                   19-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p56-lck; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2458 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAACTTTGAGGAAGAAGAAGAAGATGAAGAA 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple sclerosis allergic reactions, Crohn's diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p160 cDNA 160.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                               95US-0574959
                                                                                                                                                                                                                                                                                                                                   96WO-US19944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 439..3846
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/note= "160.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
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52.0%;
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Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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WPI; 1997-341351/31 Joung I, Shin J,

Strominger JL, Vadlamudi RK;

of.

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ABA90521/

ID ABA9

XX ABA9

XX ABA9

XX Genc

XX Genc

XX Bios

XX Lact

XX FR28

XX Lact

XX II--

XX II--

XX II--

XX II--

XX II--

XX Boll

XX Boll
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rinis cDNA sequence encodes a novel p160 (160.1) which is capable of activating transcription of a variety of genes upon activation of p62 and is capable of binding to the p62/p561pk complex to modulate Lck function in a manner similar to p62. The genes transcribed in response to p160 activation likely include those of which are involved in T or B cell development/differentiation, T or B cell activation or production of T or B cell specific factors e.g. lymphokines or antibodies. This p160 polypeptide is also a substrate for serine/threonine kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3148
   WPI; 2002-043418/06
                                                                                                                                     11-APR-2000;
                                                                                                                                                                                                      FR2807446-A1
                                                                                                                                                                                                                                                                       Biosynthesis;
                                                                                                                                                                                                                                                                                                     Genomic sequence of Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                         ABA90521 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p160 polypeptides can modulate degradation of cellular proteins e.g. celloycle regulatory proteins stimulating expression of cell cycle dependent kinase inhibitors and arresting cell cycle progression at specific boundaries to thereby modulate cell proliferation. As p160 boosts B cell response it may be used to treat disorders where this is beneficial, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. for treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding p62 and p160 and corresponding proteins - used in the treatment of autoimmune disease and for T and B cell proliferation,
                                 Bolotine A,
                                                                                                    11-APR-2000; 2000FR-0004630
                                                                                                                                                                      12-OCT-2001.
                                                                                                                                                                                                                                     Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                      16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                         ABA90521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3901 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis allergic reactions, Crohn's diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibitors could reduce B or T cell responses and may be used to variety of autoimmune diseases, e.g. diabetes mellitus, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections by pathogenic microorganisms. p160 can be used to expand cell populations for treating infectious diseases or cancer and p160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW31185
                                                                  (INRG ) INRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                            ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82; Fig 8; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                   2000FR-0004630
                                   Sorokine
                                                                  INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                     biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 A; 1183 C;
                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                       IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%;
                                 P
                                                                                                                                                                                                                                                                                                                                                                                                          2365589
                                 Renault P, Ehrlich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40.2; DB Pred. No. 0.18;
                                                                                                                                                                                                                                                                   lactic bacterium; yogurt; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1128 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           809 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | p160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   γQ
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ABA49279/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            997806 TCTTTCTGAAGA 997795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    997866 AATAGAATTACTGACAGAGCTATCAGTCACTTACAATCTTGGAAATCACGATATGGTTGG 997807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       997986
                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
Penn
                             (MOLE-)
                                                                                                                                                                              30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                       WO200157271-A2
                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                  disease; cancer;
                                                                                                                                                                                                                                                                                                               Human; microarray; single
                                                                                                                                                                                                                                                                                                                                          Human breast cell single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                       ABA49279;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA49279 standard; DNA; 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention helps research in lactic bacteria, particularly useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 1; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 CGATAAATCTTTTAAGAAGTCCTCTGATCTTGACGAATGCAAAAAAACATGTTTCAAGAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 TTCTTCAGAAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTT 116
SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATGGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACATTTTGCTGGTGATATTTCAAATGATTTTCACGGAATTTCCGAACCATTTTTCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTCAAGAAGAAATTGATATTTTTCTGTCTCTTTTAAAGGATTTAAAGATTACAGATTT 997927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and related
                             MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
Hanzel DK,
                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                  SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%;
50.5%;
Chen W,
                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; I
Pred. No. 2
   Rank DR
                                                                                                                                                                                                                                                                                                               probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                expression; breast;
                                                                                                                                                                                                                                                                                                                                            probe #7974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2365589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               997867
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RESULT 11
ABA67193/c
ID ABA671
XX ABA671
XX ABA671
XX O1-FEB
XX Human
DT Human;
XX Human;
XX Homo s
XX WO2001
XX WO2001
XX WO2001
XX O9-AUG
XX O1-FEB
PR 04-FEB
PR 04-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               controlled acid probes for measuring gene expression in a sample derived controlled acid probes with a collection of detectably labelled nucleic acids contacting controlled from many breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids controlled from many of the measuring the label controlled from many of the measuring the label controlled from the expression of regions of genomic DNA predicted to concode proteins. They are useful for gene discovery, and for cencode proteins. They are useful for gene discovery, and for cencode proteins. They are useful for gene discovery, and for concode proteins. The microarray of this invention presents a far greater concoderate on cells. The microarray of this invention presents bias than expressed sequence tag microarrays. The method is suitable for capit production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the controlled specification, but was obtained in electronic format directly from with a firm with inholynihished not sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; SEQ ID NO 7974; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
 04-FEB-2000;
26-MAY-2000;
                                    30-JAN-2001; 2001WO-US00669
                                                                                                                                             Human; foetal liver;
                                                                                                                                                                     Human foetal liver single exon nucleic acid probe #15498
                                                                                                                                                                                                  01-FEB-2002
                                                                                                                                                                                                                           ABA67193;
                                                                                                                                                                                                                                                    ABA67193 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 766
                                                                                          WO200157277-A2
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           irom WIPO at ftp.wipo.int/pub/published_pct_sequences:
                                                                                                                                                                                                                                                                                                                                                                       567
                                                                                                                                                                                                                                                                                                                                                                                                                           627
                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687
                                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                                                                                                                             367
                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                              TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                                   GA 506
                                                                                                                                                                                                                                                                                                                                             GA 368
                                                                                                                                                                                                                                                                                                                                                                      GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                               (first entry
 2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 A; 299 C; 36 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.6%;
                                                                                                                                             gene expression; single exon
                                                                                                                                                                                                                                                     766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.6; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                           probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                               366
                                                                                                                                                                                                                                                                                                                                                                                                                         568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628
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                                                                                                                                                                                                                                                                                                                                                                                 В
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04-FEB-2000; 2000US-0180312
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ABA34288/c
ID ABA342
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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Best Local (
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
30-JAN-2001; 2001WO-US00666
                                                                                                                                                            congenital heart disease;
                                                                                                                                                                            Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                           Probe #12754
                                                                                                                                                                                                                                                                                                                          ABA34288;
                                                                                                                                                                                                                                                                                                                                                                 ABA34288 standard; DNA; 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 15498; 639pp + sequence listing; English.
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                                                                               WO200157274-A2
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                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGGAGAGGATGATAATGATGACGATGATGATGATTATGATAATGATGGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived single exon nucleic acid probes useful for zing gene expression in human fetal liver -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                        for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                              (first entry)
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51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     did not form part of
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RESULT 13
AAI22114/c
ID AAI221
XX AAI221
XX AAI221
XX AAI221
XX Probe
XX Probe;
KW Probe;
KW Cervic
XX Homo s
PN WO2001
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systee.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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             09-AUG-2001
                                     WO200157278-A2
                                                                                      cervical cancer;
                                                                                                                     Probe #12047 for gene expression analysis in human cervical cell sample
                                                                                                                                                12-OCT-2001
                                                                                                                                                                        AAI22114;
                                                                                                                                                                                               AAI22114 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification,
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                                                            sapiens.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 190 A; 299 C;
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Pred. No. 0.14;
                                                                                                 expression;
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                                                                                                 cervical
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                                                                                                epithelial cell;
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ID AAI47409 standard; DNA; 766
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Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray, which can be used tot measuring ....... generally, which can be used tot measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells. By measuring generally derived from human cervical epithelial cells.
                                                                                                         Probe; microarray;
                                                                                                                                                                    17-0CT-2001
                                                                                                                                                                                                   AAI47409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 766 BP; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                      Probe #16095
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                            506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 12047; 487pp; English.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                       used
                                                                                                                                                                    (first entry)
                                                                                                                                      to measure gene expression in human placenta
                                                                                                       human;
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51.1%;
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                                                                                                       placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                         antenatal diagnosis;
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0;

WO200157272-A2

Homo

sapiens

genetic

disorder;

SS

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AAIO7812/c
ID AAIO78
XX
AC AAIO78
AC Probe
DE Probe;
KW Probe;
KW Inflan
OX Homo s
XX
WO2001
XX
PN WO2001
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PD 09-AUC
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04-FEB-2000; 2000US-0180312
                         29-JAN-2001; 2001WO-US00661.
                                                  09-AUG-2001
                                                                           WO200157270-A2
                                                                                                                        Probe; human; breast disease; breast cancer; development disorder; ss;
inflammatory disease; proliferative breast disease; non-carcinoma tumo
                                                                                                                                                              Probe #7803 used to
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03-AUG-2000;
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26-MAY-2000;
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2000US-0207456
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                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                          of the breast, fibrocystic changes, non-carcinoma tumours.
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	UT 1 48-332-463-14/c quence 14, Application US/ tent N. 5670367 ENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G TITLE OF INVENTION: RECC UMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lar STREET: 1800 Diagonal CITY: Alexandria STATE: VA COUNTRY: USA ZIP: 22313-029 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: IBM PC COMPA COUNTRY: USA ZIP: 22313-029 COMPUTER: PALENTION OPERATING SYSTEM: PC-D SOFTWARE: PATENT NO DATA: MEDIUM TYPE: Floppy di COMPUTER: 18M PC COMPA OPERATION NUMBER: US FILING DATE: 26-AUG-19 COMPUTER: PATENT NUMBER: US FILING DATE: 26-AUG-19 APPLICATION NUMBER: US FILING DATE: APPLICATION NUMBER: EP FILING DATE: APP		QQQQQQQQQQQQQ
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Matches 14; Conservative 1
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                                                                                                                                                                                      TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AAGAACGTGAAGATTGTTGGACGTTTTACGCGAACAGAAAATATACAGACTTCGATAAAT 124
                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                              NAME/KEY:
                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                LOCATION:
                                                                                                                                                        LENGTH:
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                                                                                                                                                        3211 base pairs
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                                                                                                             linear
                                              439..3157
                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                          single
                                                                                             CDNA
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AND USES THEREFOR
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70; Mismatches 123;
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Score 40.2;
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2;
Length 3211;
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                                                                                                                                                                                     US-09-357-014-8
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                                                                                                           Matches 90;
                                                                                                                                              Query Match
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                                     319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
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 259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
                                                                        199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/574,959
FILING DATE: «Unknown)
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DEN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/357,014
FILING DATE: 19-Jul-199
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 439..3157
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDE: AND USES THEREFOR
                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                               Conservative
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                                                                                                                              Score 40.2; DB 4;
Pred. No. 0.0066;
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          Sequence 6, Application US/09357014 Patent No. 6291645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                     3148 GAAGAAGAGGAAGAAGAAGAAGAAGAAGAAGAACTTTGAAGAAGAAGAAGAAGATGAAGAG 3207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: 652 POLYPEPTIDES, RELATED POLYPEPTIDE.
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
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ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                         199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                      259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
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                                                                                         APPLICANT:
                                      APPLICANT:
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     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               199 GAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCAA 258
                                                                                                                                                                                                                                                                                        319 GATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                           259 GAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAA 318
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APPLICATION NUMBER: US/09/357,014
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 439.
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                                                                                         Bohenzky, Roy A.
                                                                                                            Chang, Yuan
                                        Moore, Patrick S.
                                                        Edelman, Isidore S.
                                                                           Russo, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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(617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%;
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Pred. No. 0.0073;
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DB 4; 83;

Length 3901; Indels

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US-09-298-568-1
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                                                                                                                    GENERAL INFORMATION:
                                                                                                                                     Sequence 1, Application US/09298568 Patent No. 6322792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 057
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/728,323A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 10.6%;
Local Similarity 47.2%;
                                                                                                                                                                                                                                                                                  GAAGTTGATGAAGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAAATTAT 297
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SEQ ID NO 1
LENGTH: 3489
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Best Local Similarity
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CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ANAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Kaposi's sarcoma-associated herpesvirus
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Edelman, Isidore S.
APPLICANT: MOOTE, Patrick S.
TITLE OF INVENTION: POLYEPTIDE
TITLE OF INVENTION: HERPESVIRUS
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STATE: New Yor
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                                                                                                                                                                                                  APPLICATION NUMBER:
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5849564
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47.2%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

STRANDEDNESS:

nucleic acid

32207 base pairs

TOPOLOGY: TYPE: LENGTH:

linear

0,

double

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RESULT 9
US-08-757-669A-20/c
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                                   TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21066 GGGGACAACGAGATTAGCAAGGAAAGTCAGGTTGACAAGGATGACAATGACAATAAGGAT 21007
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                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         TELEPHONE:
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGGAGGATGACGAG 2088
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                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                     E: Cooper & Dunham LLP
1185 Avenue of the Americas
32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bohenzky, Roy A.
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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                                                                       (212) 278-0400
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                                                                                                                                                                                                                       US/08/757,669A
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Pred. No. 0
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.6%;
Best Local Similarity 47.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Edelman, Isidore S
APPLICANT: MOORE, PATTICK S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-0
                                                                                                                                                                                               21126 GAAGAAGCATCCAAGAATGAAAAAGAATGTTCCGAAAATAATCAGGCTGGCGAGGATAAT 21067
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                                      21006 GATGAGGAGGAGGAGGAGAATGAGGAGGAGGAGGATGACGAGGAGGATGACGAG 20947
                                                                                                                 21066 GGGGACAACGAGATTAGCAAGGAAAGTCAGGTTGACAAGGATGACAATGACAATAAGGAT 21007
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                           238 GATGGTGAAGAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTAT 297
                                                                                                                                                        178 GAGTACTGCTACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTT 237
                                                                                                                                                                                                                                   358 GAAGTTGATGAAGA 371
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298 TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGAT 357
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                              120;
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                                                                                                                                                                                                                                                                                                                                                                                                                  32207
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.0
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Russo, James J
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                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                          Score 39.6; DB Pred. No. 0.03; 0; Mismatches
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                                                                                                                                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                                                                                                                                               Length 32207;
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763 GA 764

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US-08-766-738-2
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Best Local S
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20946 GAGGATGACGAGGATGACGAGGATGACGAGGATGACGAGGATGACGAG 20887
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LIBRARY: Conser
CLONE: 1813361
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LENGTH: 966 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                373
                                                   703 GACGACGATGAAGTCAGTGAGGAGGAAGAAGTTTGGACTTGATGAAGAAGATGAAGAT 762
                                                                                                                      643 GGTGAAGAAGAGGAGTTTGATGAAGAAGATGAAGATGAAGATGTAGAAGGGGATGAG 702
                                                                                                                                                                                             583 GTTGATNAAGANGAGGAGGACGGAGAAGGAGGAGGAGGAAGACGAGGACGATGAGGAT 642
                                                                                                                                                                                                                              193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                        253 GACCAAGAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
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OPERATING SYSTEM:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                Match 9.6%;
Local Similarity 49.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                TA 374
                                                                      GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGTTGATGAAGA 371
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                                                                                                                                                                                                                                                                 0; Mismatches
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RESULT 13
US-08-867-941-2
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US-09-262-610-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                  643
763 GA 764
                               373 TA 374
                                                                703 GACGACGATGAAGTCAGTGAGGAAGGAAGAATTTGGACTTGATGAAGAAGATGAAGAT 762
                                                                                                                                                               253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                                                                                                                                                                                                               193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                 LIBRARY:
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                                                                                               GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                                                                                                                                                GTTGATNAAGANGAGGAGGACGAGAAGGAGGAGAAGATGAGGAAGACGAGGACGATGAGGAT 642
                                                                                                                                GGTGAAGAAGAGGAGTTTGATGAAGAAGATGATGAAGATGAAGATGTAGAAGGGGATGAG 702
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49.5%;
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Pred. No. 0.077;
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                                                                                                                                                                 RESULT 14
US-09-074-658-2
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Best Local Similarity 52.2%;
Matches 105; Conservative
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                                                GENERAL INFORMATION:
APPLICANT: LOOSMORG
APPLICANT: Run-Pan
APPLICANT: Quijun |
                                                                                                                          Sequence 2, Application US/09074658 Patent No. 6184371
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APPLICANT: LOOSMO
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INFORMATION FOR SEQ ID NO: 2:
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CORRESPONDENCE ADDRESS:
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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2191 TCACAAGATGATGACGCAGAT 2211
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FITLE OF INVENTION:
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ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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EDNESS: single
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Yang, Yan-Ping
Klein, Michel H
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               Quijun Wang
Yang, Yan-Ping
Klein, Michel H
                                                                        Run-Pan Du
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LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                         Sheena M
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Pred. No. 0.25;
0; Mismatches
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US-08-867-941-1
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT:
APPLICANT:
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
                                                                                                                                                TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 67
                                                                                                                               CORRESPONDENCE ADDRESS:
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CITY: Toronto
STATE: Ontario
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Local Similarity 52.2%;
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                                                                            CITY: Toronto
                                                                                             STREET:
                                                                                                               ADDRESSEE:
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Yang, Yan-Ping
Klein, Michel H
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SYSTEM: PC-DOS/MS-DOS
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 Mismatches

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Search completed: May 5, 2003, 17:46:42 Job time: 76 secs
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
AMME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELEPHONE: (416) 595-115
FELECOMMUNICATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7650 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
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||| || || || || || || || || 2331 TCACAAGATGATGACGCAGAT 2351
                                                                                                                                                                                                                                                                                                                                                  2271 TCTGATGATTCACAAGATGATGATGCACATGGCGATGATGATTTGATTGCATCTGATGAT 2330
                                                                                                                                                                                                                                                           2217 TATCTGTTAACCGAAGACTTCACCCCAGAA-----GATGATGACGATGATTTGACCGCA 2270
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Result.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 87, Appl	e 4012		Sequence 3, Appli	Sequence 592, App		Sequence 33, Appl			Sequence 23266, A	Sequence 2534, Ap	Sequence 19262, A	•	Sequence 9281, Ap	Sequence 20, Appl	Sequence 21610, A	Sequence 8451, Ap	Sequence 89, Appl	œ	Sequence 1, Appli		Sequence 3, Appli	Sequence 12239, A	Sequence 4988, Ap		Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-09-918-995-348 US-09-918-995-348 Sequence 348, Application US/09918995 Sequence 348, Application US/09918995 PUBLICANT: MYSEQ INC. FILE REFERENCE: 20411-756 FILE REFERENCE: 20411-756 CURRENT PLING DATE: 1999-01-20 NUMBER OF SEQ ID NO. 348 SEQ ID NO. 348 SEQ ID NO. 348 LENGTH: 462 FEATURE: NAME/KEY: misc_feature LOCATION: (10)(462) OTHER IMPORMATION: n = A,T,C or G SOTURNE: MRORMATION: n = A,T,C or G UNIVERSOR SEQ ID NO. 348 LENGTH: 452 COLUMNE: MSC_feature LOCATION: (1)(462) TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (1)(462) OTHER IMPORMATION: n = A,T,C or G USC-09-918-995-348 OUGHY MATCH OUETY MATCH Best Local Similarity 50.5%; Pred. No. 0.11; Best Local Similarity 60.5%; Pred. No. 0.11; Best Local Similarity	-	 	
		Query Match 10.6%; Score 39.6; DB 9; Length 462; Best Local Similarity 50.5%; Pred. No. 0.11; Matches 96; Conservative 0; Mismatches 94; Indels 0; Gaps	pplication US/09918995 US20030073623A1 TION: eq Inc. TION: NOVEL NUCLEIC ACID SEQUENCES TION: FROM VARIOUS CDNA LIBRARIES : 20411-756 ATION NUMBER: US/09/918,995 DATE: 2001-07-30 ION NUMBER: US/09/235,076 ATE: 1999-01-20 ID NOS: 38054 SEQ for Windows Version 3.0 o sapiens c_feature(462) TION: n = A,T,C or G

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OTHER INFORMATION: EXPRESSED IN BE7474,
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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CURRENT FILING DATE: 2001-05-23
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/207,456
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R OF SEQ ID NOS: 49117
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APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2000-10-04
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APPLICATION NUMBER: US 09/632,366
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HIT: AW844901.1, EVALUE 2.90e+00
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IN FETAL LIVER, SIGNAL = 1.2
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HBL100, SIGNAL = 1.1
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NUMBER OF SEQ ID NOS: 49117
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                          Sequence Listing Engine vers. 1.1
                                                                                                                                                                                               2001-01-30
                                                                                                                                                                                                                           2001-01-30
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                                                                                             2000-06-30
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                                                                                                                                                                                                             PCT/US01/00661
                                                                                                              US
                                                                                                                                              US 60/234,687
                                                                                                                                                                                                                                                                              PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                               PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04
                                                                           09/774,203
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21723, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                 PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron G.
                                              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO AL008720.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 TACATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                           APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGAGGGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGAGAGGATGATAATAATGATGACGATGATGATGATTATGATAATGATGGGGAGGAG 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGTTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGAC 306
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OTHER INFORMATION: MAP TO ALO33533.5

OTHER INFORMATION EXPRESSED IN HEALON, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HEALON, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN BI474, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4

OTHER INFORMATION: NT HIT: U28921.1, EVALUE 6.50e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-783-590-5790

; Sequence 5790, Application US/09783590

; Patent No. US20020110850A1
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: DS060/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER: US 09/774,203
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                                                                                                                   CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                                                                                                       APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, Willia APPLICANT: Li, Haodong
                          PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
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SOFTWARE: Annomax Sequence Listing Engine vers.
SOFTWARE: PatentIn Ver.
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 GAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 ATCGTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 TTAGACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 9.9%;
Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                 Haseltine, William A.
Li, Haodong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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CCATION: (337)

COCATION: (337)

OTHER INFORMATION: n equals a,t,g, ou NAME/KEY: misc feature
LOCATION: (345)

OTHER INFORMATION: n equals a,t,g, ou NAME/KEY: misc feature
LOCATION: (346)

OTHER INFORMATION: n equals a,t,g, ou NAME/KEY: misc feature
LOCATION: (348)

OTHER INFORMATION: n equals a,t,g, ou NAME/KEY: misc feature
LOCATION: (348)

OTHER INFORMATION: n equals a,t,g, ou NAME/KEY: misc feature
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LENGTH: 499
                                                                 NAME/KEY: misc feature
LOCATION: (396)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (127)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (211)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (9)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                             LOCATION: (394)
OTHER INFORMATION: n equals
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LOCATION: (375)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (330)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (320)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (302)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                 OTHER INFORMATION: n equals a,t,g,
                                                                                                                                        OTHER INFORMATION: n equals
                                                                                                                                                           NAME/KEY: misc feature LOCATION: (395)
                                                                                                                                                                                                                                  OTHER INFORMATION: n equals NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature LOCATION: (388)
                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (368)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (337)
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misc feature (408)
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RESULT 6
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Best Local
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (423)
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OTHER INFORMATION: n equals a,t,g, or
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                                                           130 CATTTCATGTAATTACCTTTTAATTTGAACATTTAGAACATGCTGTTAGATG 181
                                                                                               151 GAATGCAAAAAAACATGTTTCAAGACGGAGTACTGCTACATCGTTTTTGAAG 202
                                                                                                                                                               91 TACGCGAACAGAAAATATACAGACTTCGATAAATCTTTTAAGAAGTCCTCTGATCTTGAC 150
                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                      31 CTCGCAAGCTTGCTGATCTCAACTACTTCTTCAGAAGAACGTGAAGATTGTTGGACGTTT 90
                                                                                                                                      TCCCAGCACAAAAGAGATTGTCTTAGATAAGACAGTAAAGAGAATTGTATATCATNAT 129
                                                                                                                                                                                                                                                                                         87;
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                                                                                                                                                                                                                                                                                           Score 36.6; DB 10;
Pred. No. 0.82;
0; Mismatches 85;
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Gaps

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US-10-015-219-700

Sequence 700, Application US/10015219 Publication No. US20030008299A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1

CURRENT APPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02

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; NAME/KEY: misc_feature
; LOCATION: 66, 201, 213, 225, 251,
; LOCATION: 313, 322, 339, 373
; OTHER INFORMATION: n = A,T,C or G
US-10-015-219-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-777-564-700
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SEQ ID NO 700
LENGTH: 381
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 700
LENGTH: 381
TYPE: DNA
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 700, Application US/09777564 Patent No. US20020022591A1
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CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (1)...(381)
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                    193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGAAGGGGTA 252
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Local Similarity 49.5%;
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                                 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
                                                                       GGTGAAGAAGAGGAGTTTGATGAAGAAGATGATGAAGATGTAGAAGGGGGATGAG
                                                                                                         GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG
   GACGACGATGAAGTCAGTGAAGGAAGGAAGAATTTGGACTTGATGAAGAAGAAGAAT
                                                                                                                                             GTGGATGAAGAGGAGGAGGACGAAGAAGAAGAAGATGAGGAAGACNAGGACGATGAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Window Version 4.0
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                                                                                                                                                                                                                 Score 36; DB 10; Length 381; Pred. No. 1.1; O; Mismatches 92; Indels
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763 GA 764
                                 373 TA 374
                                                                     703 GACGACGATGAAGTCAGTGAGGAGGAAGAAGTTTGGACTTGATGAAGAAGATGAAGAT
                                                                                                                                                                             253 GACCAAGAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAG 312
                                                                                                       313 GGTAAAGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAGAT 372
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                                                                                                                                                                                                                                                                                       90;
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Sequence 2, Application US/10213700 Publication No. US20030022332A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
193 GTTTTTGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF-0177 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHATASE INHIBITOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                         Similarity
                                                                                                                                                                       CLONE: 1813361
                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/766,738 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/213,700 FILING DATE: 06-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                      LIBRARY: Consensus
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                                                     Conservative
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LENGTH: 204
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
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HER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
HER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
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HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
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APPLICATION NUMBER: US 09/774,203
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                                           BE889896.1, EVALUE 2.80e+00
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RESULT 10
US-09-864-761-4255/c
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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Matches 73;
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SEQ ID NO 4255
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CURRENT FILING DATE: 2001-05-23
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                                    SOFTWARE: Annomax Sequence
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APPLICATION NUMBER:
FILING DATE: 2001-01
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Chen, Wensheng
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                                                  US-09-770-445-544
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                                                                                                    SEQ ID NO 544
LENGTH: 876
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 544, Application US/09770445
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                             APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
FILE REFERENCE: 2023US (PARA-012PRV)
                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                     SOFTWARE:
                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                    PRIOR FILING DATE:
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OTHER
OTHER
                                                                ORGANISM: Arabidopsis thaliana
                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 GATGAAAATGAAGAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 GAAGTTGATGAAGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 TTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCCAGGTACAGGTGACGAGTCAGAT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 GATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                     FastSEQ for Windows Version 4.0
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Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                                                                                                                        Allen, Keith
                                                                                                                                                                                                                                                                                                                                    Davis, Keith R.
                                                                                                                                                                                                                                                                                                                                                                                                       Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu, Yang
Rameaka, Joshua G.
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Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matthew,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An, Yong-Qiang
Hamilton, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raines, Tracy M.
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N: EXPRESSED IN HEART, SIGNAL = 1.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

N: EXPRESSED IN BAIN, SIGNAL = 1.5

N: EXPRESSED IN BAIN, SIGNAL = 1.6

N: EXPRESSED IN HONE MARROW, SIGNAL = 1.6

N: EXPRESSED IN HELA, SIGNAL = 1.6

N: EXPRESSED IN HELA, SIGNAL = 1.9

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7
                                                                                                                                                                    2000-01-27
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                                                                                                                                                                                  2001-01-26
BER: US 60/178,472
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9.4%;
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Score 35.4; D
Pred. No. 2.4;
               DB 10;
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                 Length 876;
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RESULT 13
US-09-878-574-15076
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
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                                                                                                                                                                                                                            Sequence 15076, Application US/09878574 Patent No. US20020110548A1
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LENGTH: 1092
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                               941 TTGTGTATAAACTGAAAGAAATGGGTAAGATTGATGAGAAAGATATTTCTGGGATAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  881 ACAATGATCTCGAAGCAGCTGATCTCGATGAAGATGGAGTTGTTGGAGCTGCAGAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 ACAATGTCGTTGATGGTGAAGAGTTAGACCAAGAAAAATTTGTTGTCGACGAAAACTTCA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 TTGTGTATAAACTGAAAGAATGGGTAAGATTGATGAGAAAGATATTTCTGGGATAATGG
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                                                                                                                                                                                                                                                                                                                                                           ATGAGTTCGAGCAACTTGATTACGATGAA 1029
                                                                                                                                                                                                                                                                                                                                                                                                   ACGAGTCAGATGAAGTTGAAGATTAA 375
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52.3%;
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Pred. No. 2.
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; Prior Application removed - Se; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 332; LENGTH: 520; TYPE: PRT : ORGANISM: Homo Sapien
US-10-184-644-332
                                                           RESULT 15
US-10-184-634-332
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US-10-184-644-332
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Baul
APPLICANT: Gurney, Austin
APPLICANT: Pan, James
Sequence 332, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 15076
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No.
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CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 GGTACAGGTGACGAGTCAGATGAAGTTGAAGATTAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 GAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAAAGATGCAGGTAATGCGGCA 336
                                                                                                                                                                               318 AGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGATGAAG 370
                                                                                                                                                                                                                       165 PGAPGPPGPPAEKGAKGAMGRDGATGPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGP
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                                                                                                                                         225 QGEKGSKGDGGLIGPKGETGTKGEKGDLGLPGSKGDRGMKGDAGVMGPPGAQG
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Godowski, Paul J.
Gurney, Austin L.
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
LENGTH: 520
TYPE: PRT
ORGANISM: Homo Sapien
US-10-184-634-332
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Search completed: May Job time: 142 secs
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
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Godowski, Paul
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Maximum DB seq length: 2000000000
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BM168486 EST571009
BM165474 EST567997
AZ688514 ENTM022TF
BM163498 EST566021
BM166089 EST568612
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KEYWORDS
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AUTHORS
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ALIGNMENTS

LOCUS

AZ550718

DEFINITION

ENTEMN36TF Entamoeba histolytica Sheared DNA Entamoeba histolytica Sheared DNA Entamoeba histolytica Sequence.

ACCESSION

AZ550718

VERSION

KEYWORDS

SOURCE

ORGANISM

Entamoeba histolytica.

DRATESO718.1 GI:11176019

GSS.

Entamoeba histolytica.

ENTEMNENT

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I (bases 1 to 879)

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Department of Enkaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3543

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica High quality sequence stop: 801.

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BASE COUNT
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                          Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
                                                                                                                                                                                                      1 (bases 1 to 701)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
                                                                                                                                                                                                                                                        Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                   Contact: Jane Carlton
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/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
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RESULT 3
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EST567997 PyBS Plasmodium yoelii yoelii cDNA clone PYCMN68
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Seg primer: ADF.
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9712 Medical Center Drive, Rockville, Tel: 301-530-9319
Fax: 301-838-0208
                                                              Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
                                                                                                                                                                                     1 (bases 1 to 721)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W.,
Fraser,C.M. and Carucci,D.J.
                                                                                                                                                                                                                                                   Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Plasmodium yoeliata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                      Plasmodium yoelii EST project at TIGR Unpublished (2001)
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pBD-GAL4, At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL
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                                                                                                                                                               1 (bases 1 to 881)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:MSS sheared DNA library
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Seq primer: ADF.
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For clone info, please contact the Malaria Research and Reference
                                                                                              Department of Eukaryotic Genomics
                                                                                                                          Contact: Brendan J Loftus
                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                      Eukaryota; Entamoebidae; Entamoeba.
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                                                                          Institute for Genomic Research
Medical Center Dr., Rockville,
301 838 0208
301 838 3543
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/lab_host="E. coli XL-1 Blue"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/CBJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method,
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                  EST.

Plasmodium yoelii yoelii.

Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Clones are derived from the Entamoeba histolytica HMl:IMSS sheared
                                                                                                                                                                                             BM163498
BM163498.1 GI:17309179
                                                                                                                                                                                                                                                                      EST566021 PyBS Plasmodium
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/note="Yector: pHOS1; Site_1: Bst I; Constructed at The
/note-"Yector: pHOS1; Site_1: Bst I; Constructed at Dismond Clark,
Genomic DNA isolated from broth cultures of E, histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Pred. No. 0.00059;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

[ (bases 1 to 272)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B., Eraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                              BM166089 272 bp mRNA linear EST 04-DE EST588612 PyBS Plasmodium yoelii yoelii cDNA clone PYCNC52 5'
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       Plasmodium yoelii EST project at TIGR
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Plasmodium yoelii yoelii
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Contact: Jane Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: ADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: carlton@tigr.org
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The Institute for Genomic Research
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/lab_host="E. coli XI-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanddinium isothiocyanate method, and
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Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project at
                                                  Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
                                                                                                                    Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
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Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
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Fax: 301-838-0208
                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 274)
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/lab_host="E. coli XL-1 Blue"
/note="Vector: par-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL
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  1 (bases 1 to 276)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelli EST project at TIGR
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
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Fax: 301-838-0208
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Contact: Jane Carlton
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guandinium isothiocyanate method, and
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1 (bases 1 to 425)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Parasite Genomic Genomic Research
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Contact: Jane Carlton
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Plasmodium yoelii EST project at TIGR
                 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
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//note="vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiccyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-tractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
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Pred. No. 0.0011;
0; Mismatches 80
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Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                    Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                  BM171330.1 GI:17304562
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198 TGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCA 257
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1 (bases 1 to 459)
Carlton,J.M., Daly.T.M., Long.C.A., Bergman,L.W., Vaidya,A.B Fraser,C.M. and Carucci,D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM171330 A59 bp mRNA linear EST 04-DEC-2001 EST573853 PyBS Plasmodium yoelii yoelii cDNA clone PYCQT11 5' end,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.malaria.mr4.org/mr4pages/index.html
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//dev_stage="Asexual blood stages"
//lab_host="E. coli XL-1 Biue"
//note="vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanidinium isothicoyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybriZAP vector and plasmid DNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
1 (bases 1 to 580)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B. Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                             BM161175 580 bp mRNA linear EST 04-DEC-200 EST563698 PyBS Plasmodium yoelii yoelii cDNA clone PYCKB54 5' end
                                                                                                               Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                  mRNA sequence.
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Contact: Jane Carlton
Parasite Genomics Group
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For clone info, please contact the Malaria Research and Reference
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// All_host="E. coli XL-1 Blue"

// Alb_host="E. coli XL-1 Blue"

// All_host="E. coli XL-1 Blue"

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Similarity 55.1%;
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318 AGATGCAGGTAATGCGGCAGGTACAGGTGACGAGTCAGATGAAGTTGAAGATTAA 375
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Eukaryota; Âlveolata; Apicomplexa; Haemosporida; Plasmodium.

1. (bases I to 648)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B., Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
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Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
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Pred. No. 0.0012;
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 651)
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blo
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microcrystalline cellulose collumns. Total RNA was
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Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301-530-9319
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Contact: Jane Carlton
                   Carlton, J.M., Daly T.M., Long, C.A., Bergman, L.W., Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                           BM161293 667 bp mRNA linear EST 04-DEC-2001
EST563816 PyBS Plasmodium yoelii yoelii cDNA clone PYCKD09 5' end,
Plasmodium yoelii EST project at TIGR
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/lab_host="E. coli XL-1 Blue"
/lab_most="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
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                                             Vaidya, A.B.,
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Search completed: May 5, 2003, 17:45:16 Job time: 1581 secs
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                                                                                                                                                                                                                                                                                                                                 198 TGAAGACACGGTCAACAAGGAATGTTACTACAATGTCGTTGATGGTGAAGAGTTAGACCA 257
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                                                                                                                                                                                                                                                                      258 AGAAAAATTTGTTGTCGACGAAAACTTCACGGAAAATTATTTGACAGACTGCGAGGGTAA 317
                                                                                                         Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
The Medical Center Drive, Rockville, MD 20850, USA
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
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/dev_stage="Asexual blood stages"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BAIB/CByJ mice infected with Py17XL collected from BAIB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidnium isothicyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated."
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/db_xref="taxon:73239"
/clone="PYCKD09"
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Mouse Ice-4 protei
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Human interleukin-
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Murine caspase-12
                                                                                                                                                               S. frugiperda immu
                                                                                                                                           Drosophila melanog
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Leech antiplatelet
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734 22 734 22 738 22 635 23 1869 22 146 23 146 23 146 23 147 20 903 22 903 22 961 22 961 22 961 22 450 21 450 21 488 21	1154 22 175 21 256 21 320 21 589 22 156 23 367 22 669 23 1167 22 674 23 3257 22 717 22 734 22
	ABB66916 AAG17789 AAG17789 AAG1783 AAB10263 AAB95086 AAB95086 AAB97951 ABB71954 ABB09771 ABB09771 ABB09771 ABB09776 ABB097656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656 ABB675656
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ALIGNMENTS

RESULT 1
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AC AAY9

AAY94746 standard; Protein; 103 AA.

AAY94746;

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N-PSDB; AAA28180.	WPI; 2000-611629/58.		1	Strittmatter W, Guessow D, Hofmann U, Hemberger J, Fotev Z;		(MERE) MERCK PATENT GMBH.		12-MAY-1999; 99EP-0109503.	18-MAR-1999; 99EP-0105530.		10-MAR-2000; 2000WO-EP02117.		28-SEP-2000.		WO200056885-A1,		Hirudo medicinalis.		posterior capsule opacification.	collagen-dependent platelet adhesion inhibition;	Saratin; medicinal leech; thromboembolic disease; intraocular lens;		Platelet binding inhibitor protein Saratin amino acid sequence.		29-JAN-2001 (first entry)	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  platelet adhesion. The invention includes polynucleotide sequences encoding Saratin, an expression vector comprising the DNA sequence, host cell transformed with the expression vector, antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for modifying intraocular lenses in order to lessen the thrombogenecity of the lens material, for contacting the lens material for covalent crosslinking to modify the lens material. The lens material is used for refractive anterior or posterior chamber ocular implants, which may be implanted into the eye. This new type of coating avoids problems contributed by stimulated cell growth. In combination with other medicaments that are for instance conferring cell death, Saratin coating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 41; 46pp; English.
                                                                                                                                                                            LAPP; collagen; platelet aggregation; antithrombotic; anticoagulant; coronary artery disease; cerebrovascular disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    helps to completely overcome posterior capsule opacification. The antibody immunospecific for Saratin, as well as Saratin itself, are useful for measuring samples derived from host cell cultures or from a treated subject. The present sequence represents the amino acid sequence
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             15-APR-1992.
                                                                                                                                                                                                                   Leech antiplatelet protein.
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                                                                                                                Peptide
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/note= "21 hydrophobic
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                                                             /label= mature_protein
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Pred. No. 2.3e-52;
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LAPP blocks stimulation of platelet aggregation by collagen, at an antithrombotic concentration of about 100 nMolar (or 1.6 ug/ml). Platelet aggregation is stimulated by 2 ug/ml collagen and addition of LAPP inhibits this with an IC50 of 45nM, but this may be overcome by the addition of 0.25 mM arachidonic acid. LAPP could be used for treatment and prevention of thrombotic LAPP could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapp could be used for treatment and prevention of thrombotic lapper could be used for treatment and prevention of thrombotic lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of thrombotic lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for treatment and prevention of the lapper could be used for the lapper could be used for the lapper could be used for the lapper could be used to the lapper coul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
AAB14260
ID AAB1
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              Yuan
                                           (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                     Mus sp
                                                                                                                                                                                                                                                                                                                            Mouse
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Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL18176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                     ced-3; virally induced cell death; apoptosis; gene therapy; neural;
muscular degenerative disease; myocardial infarcation; stroke; agin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                  04-JUL-2000
                                                                                                                              US6083735-A
                                                                                                                                                                                                                                                                                                                                                    09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                               AAB14260;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB14260 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 36393; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL13970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000;
11-JUL-2000;
                                       10-JUN-1994;
                                                                                                                                                                                                                   interleukin-1beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 --LDKLRAVATSSDSDENYNKSSSPDLALDLHASDVEADVDGDEAGDADEDGDADAD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KYTDFDKS-----FKKSSDLDECKKTCFKTEYCYIVFE---DTVNKECYYNVVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EELDQEKEVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYTDADESVSAPTEFLAEFLSAVMLKDYKKA---LKYCKLILQYEPDNATAKEFYPLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           solated nucleic acid from Drosophila and
                                                                                                                                                                                                                                                                                                      Ice-4 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-191637P
2000US-0614150
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9308-0080850
                                         94US-0258287
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                                                                                                                                                                                                                 converting enzyme; ICE; cysteine protease; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DENFTEN-----YLTDCEGKDAGNAAGTGDESDEVDED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     댠
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                         418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77; DB 22; Length 368; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n part of the printed format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                     aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 6
AAY50109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a mouse ICe-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequences of human ICe-ced 3 homology (ICh-1) (AAB14253), murine interleukin-lbeta converting enzyme (mICE) (AAB14249), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed cell death (apoptosis). ICh-1 may play an important role in both the positive and negative regulation of apoptosis. The ICh gene may be used in gene therapy in disorders characterised by cell death e.g. neural and muscular degenerative diseases, myocardial infarcation, stroke, virally induced cell death and diseases, myocardial infarcation, stroke, virally
                                                                                                                                                                                                                                           regulation; proteolytic cascade; malignant condition; premalignant condition; solid tumour; lymphoma; chronic lymphocytic leukaemia; prostatic hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human Ich-1L and Ich-1S proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                      Cleavage-site
                                                                                                                                                                                Key
                                                                                                                                                                                                                         preneoplastic ds.
                                                                                                                                                                                                                                                                         Caspase; splice variant; truncated; programmed cell death;
                                                                                                                                                                                                                                                                                                Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 17; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction or stroke
                                                                         14-APR-1999;
                                                                                                                 WO9952925-A1
                                                                                                                                                                     Cleavage-site
                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                                            AAY50109 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                    16-APR-1998;
                                                                                              21-OCT-1999
                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                     21-JAN-2000
                               (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                   sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DE-----SDEVD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                EQLSLQFSNDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                caspase-12 splice variant, caspase-12L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
          Morishima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                 liver focus; chemotherapy resistance; autoimmune disease
                                                    98US-0081962
                                                                         99WO-US08064
                                                                                                                                      /note= "(
318:.319
                                                                                                                                                          Location/Qualifiers 94..95 95..419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%;
                                                                                                                                               "Caspase-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.5;
Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                          apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                AAB14259
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
WPI; 2000-464343/40.
N-PSDB; AAA72843.
                              Yuan J,
                                                   (GEHO)
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This sequence represents a cDNA encoding murine caspase-12L, a splice carriant of caspase-12. Caspases are a family of proteins involved in the regulation of apoptosis and are synthesised as proforms which are activated via cleavage after specific Asp residues. Mammalian cells carpases several caspases, and it is thought that these act in a complete protein carried to cause programmed cell death. Nucleic acids canding caspase-12s (AAZ32644) or truncated forms of caspase-12L (AAZ32667) are used for production, recombinantly or in vivo, compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death to cappase-12 polypeptides which induce programmed cell death to compare the caspase-12 polypeptides which induce programmed cell death. This is compared to the caspase-12 polypeptides which induce programmed cell death to cappase-12 polypeptides which induce programmed cell death to cappase-12 polypeptides (for example, to determine gene expression and to core expression libraries) or as molecular weight markers. Fragments core cappase-12 gene (and its allelic variants); in fluorescent in situation of the caspase-12 gene, and for characteriants are cappase-12 gene, and for core cappase-12 gene, and core cappase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ced-3; virally induced cell death; apoptosis; gene therapy; neu
muscular degenerative disease; myocardial infarcation; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse Ice-4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ32645
24-JUN-1993;
                                                                            10-JUN-1994;
                                                                                                                                                             04-JUL-2000
                                                                                                                                                                                                                                              US6083735-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB14259 standard; Protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-620369/53
                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-1beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 EQLSLQFSNDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA;
9308-0080850
                                                                            94US-0258287.
                                                                                                                                                                                                                                                                                                                                                                                                            converting enzyme; ICE; cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                            protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neural;
                                                                                                                                                                                                                                                                                                                                                                                                                    mouse
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Miura M;

GEN HOSPITAL CORP

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RESULT 8
AAB29108
ID AAB2
XX AAB2
XX AAB2
XX MUS
KW MOUS
KW CANC
XX MUS
XX WO20
PN WO20
PN 12-C
XX O6-A
XX (HAF
XX WPI;
XX WPI;
XX The
CC CAS!
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The present invention is concerned with methods for identifying compounds useful for modulating caspase-mediated apoptosis. These include the caspase-12 protein shown here. These agents can be used in the treatment
                                                                                                     Caspase-12 polypeptide useful for treating apoptotic conditions e.g. stroke, ischemia and proliferated disease e.g. cancer, lacks at least amino acids in a specific region of the native amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a mouse Ice-4 protein sequence. The present sequence was used in a sequence homology comparison with the protein sequence of human Ice-ced 3 homolog (Ich-1) (AAB14253), murine interleukin-lbeta converting enzyme (mICE) (AAB14249), murine ICE2 (AAB14252) and C. elegans ced-3 (AAB14246). The coding sequence of the present sequence is a member of a family of genes involved in programmed cell death (apoptosis). Ich-1 may play an important role in both the positive and negative regulation of apoptosis. The Ich gene may be used in gene therapy in disorders characterised by cell death e.g. neural and muscular degenerative diseases, myocardial infarcation, stroke, virally
                                                                      Claim 1; Page 65-66; 70pp; English
                                                                                                                                                                                                                                                                                                                      06-APR-2000; 2000WO-US09173.
                                                                                                                                                                                                                                                                                                                                                                                           WO200059924-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; caspase-12; calpain; apoptosis; cell death; autoimmune disease; cancer; viral infection; apoptotic condition; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine caspase-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human Ich-IL and Ich-IS proteins for negative and positive regulation of programmed cell death and for developing therapeutic methods for diseases and conditions characterized by cell death, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB29108 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 16; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myocardial infarction or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  induced cell death and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQLSIQFSNDEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                Nakagawa T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                   99US-0127967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 75.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419
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RESULT 9
AAR66769
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Best Local
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                                                                                  homolog (Ice-4), increasing Ice-4s enzymatic activity can promote the programmed cell death of cancer cells (pref. those overexpressing the bcl-2 oncogene), this can be used as the basis of a new cancer treatment. Alternatively by reducing Ice-4s enzymatic activity programmed cell death can be inhibited, this may be useful in the development of new cell lines which remain viable in culture
                                                                                                                                                                                                                                             Promoting or preventing programmed cell death in vertebrate cells - by inhibiting the activity of interleukin-1 beta converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of apoptotic conditions, including stroke, neurodegeneration, ischaemia, Alzheimer's disease and muscular dystrophy, and proliferative diseases such as cancer, autoimmune disorders such as systemic lupus erythematosus and multiple sclerosis, and viral infections, particularly those associated with herpes virus, poxvirus and adenovirus. The treatment may
                                             Sequence
                                                                                                                                                                    AAQ79969 encodes AAR66769 human interleukin-1 beta converting enzyme
                                                                                                                                                                                                   Claim 24; Fig 16; 116pp; English.
                                                                                                                                                                                                                               enzyme.
                                                                                                                                                                                                                                                                                                                                 Miura M, Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oncogene bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human interleukin-1 beta converitng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interleukin-1 beta convering enzyme homolog (Ice-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9500160-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR66769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR66769 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ
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                                                                                                                                                                                                                                                                                                     1995-051742/07
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    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             form of gene therapy.
                                             432
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                                                                       or indefinite periods,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                      93US-0080850
                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US06630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             programmed cell death;
13.2%; Score 75.5; 35.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75.5;
Pred. No. 1:
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                                                                     independant of growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme homolog; Ice-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                ВВ
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              16;
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              Length 432;
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                                                                                                                                                                                                                                           converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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Matches

Conservative

14;

Mismatches

Indels

19;

Gaps

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RESULT 10
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Best Local :
                                                                                                       Matches
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apoptosis; interleukin-1 beta converting enzyme; gene therapy.
                                                                                                                                                                                                                                                              Ich-3 (AAR98464) causes programmed cell death and shows significant homology to mouse interleukin-1 beta converting enzyme (ICE), mouse mIch-2 (AAR98461) and human Ich-1 (AAR98462-63). Its sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9620721-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine Ich-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR98464 standard;
                                                                                                                                                                                activity of ICE.
                                                                                                                                                                                                           cDNA library. The protein can be obtd, from host cells contg. vectors that include an Ich-3 coding sequence. It can be used to control the programmed cell death of vertebrate cells, to develop cell
                                                                                                                                                                                                                                                                                                                    Claim 24; Fig 14; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Preventing or promoting programmed cell death in vertebrate cells comprises inhibiting or increasing the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miura M, Yuan J;
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                          interleukin-1-beta converting enzyme, or altering expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                ines that remain viable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
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96 EQLSIQFSNDEDD 108
                          95
                                                   40
                                                                         44 VFEDTVNKECYXNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                    deduced from the Ich-3 gene (AAT31554) isolated from a mouse thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
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                                                                                                                                                                                                                                                                                                                                                                                                              1996-333763/33:
DB; AAT31554.
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                          DE-----SDEVD 101
                                                   VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 95
                                                                                                       26;
                                                                                                                    Similarity
                                                                                                                                                         432 AA;
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0368704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US00177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 432 AA
                                                                                                                  13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP
                                                                                                                                                                                                for extended periods, and to increase the
                                                                                                      14;
                                                                                                   Score 75.5; D
pred. No. 14;
14; Mismatches
                                                                                                                                DB 17;
                                                                                                      14;
                                                                                                                               Length
                                                                                                       Indels
                                                                                                       19;
                                                                                                                                                                                                                                                                   sequence
                                                                                                      Gaps
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RESULT 11 ABB66916

Protein identification; signal transduction pathway; metabolic pathway;

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RESULT 12
AAG17789
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL/16-ABL/3611), expressed DNA sequences (ABL/16-ABL/36175) and the encoded proteins (ABB/7037-ABB/7072).
                      Arabidopsis thaliana protein fragment SEQ ID NO: 18943.
                                                                                                      AAG17789 standard; Protein;
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 27540; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB66916 standard; Protein;
                                                                             AAG17789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                   17-OCT-2000
                                                                                                                                                                                                                       505 SKKDIDESKEESMLDDKDKLKERVAELMVRCMFLMEKRMQQDLKGNKVCNVEEKDNNVNQ 564
                                                                                                                                                                     565 LVENFWRHYIQCCECQKKDACALSNPSMLGNTEYTG 600
                                                                                                                                                                                                                                                 12 NRKYTDFDKSFKKSSDLDECK-KTCFKTEYCYIVFEDTVNKECYYN-VVDGEELDQEKFV 69
                                                                                                                                                                                              70 VDENFTENYL--TDCEGKDA-----
                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-656860/75.
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                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                 1154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                           Conservative
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                                                 (first entry)
                                                                                                                                                                                                                                                                                         12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , dwd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting 1000\ \mathrm{or} more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                              14;
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                                                                                                        175
                                                                                                                                                                                                                                                                                           Score 73.5;
Pred. No. 73;
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                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                               42;
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                                                                                                                                                                                                                                                                                                       Length 1154;
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8	XX PN XX XX XX
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2000EP-0301439. 99US-01231825. 99US-0123548. 99US-0125788. 99US-0126785. 99US-0126785. 99US-0126785. 99US-013644. 99US-0130047. 99US-0130097. 99US-013344. 99US-013344. 99US-013344. 99US-013344. 99US-013348. 99US-013348. 99US-013348. 99US-0133476. 99US-013476. 99US-01346. 99US-01346. 99US-013945.	n assay; genetic mapping; gene sequence. thaliana.
	expression control; promoter;
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RESULT 13
AAG17788
ID AAG177
XX AAG17
XX AAG17
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DX Arabi
XX Prote
KW Prote
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              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1999;
14-OCT-1999;
                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 18942.
                                                                                       17-OCT-2000
                                                                                                                 AAG17788;
                                                                                                                                       AAG17788 standard; Protein; 256
                                                                                                                                                                                                    142
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                                                                                                                                                                                                                                                KKGS-----KRALPEESFFTWFTDAQHKE-----DAGDEIHDEVADIIKEDLWSNPLTY 141
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l Similarity 28.6%;
26; Conservative 1
                                                                                       (first entry)
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990S-0153758
990S-0154018
990S-0154779
990S-01555486
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990S-0157717
990S-0157763
990S-0159339
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990S-0160741
990S-0160761
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Pred. No. 12;
12; Mismatches
                                                                                                                                        AA.
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  08-JUN-1999;
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16-JUN-1999;
16-JUN-1999;
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30-APR-1999;
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05-MAY-1999;
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05-MAR-1999
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15-JUL-1999; 16-JUL-1999;

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RESULT 14
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AC AAB18
XX O7-NC
XX Plasm
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14-OCT-1999;
14-OCT-1999;
          WO200025728-A2
                                                 Plasmodium falciparum; antimalaria; malaria;
                              Plasmodium falciparum
                                                                              Plasmodium falciparum chromosome 2 related protein SEQ ID NO:120.
                                                                                                    07-NOV-2000
                                                                                                                        AAB18263;
                                                                                                                                            AAB18263 standard; Protein; 320 AA.
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18-0CT-1999;
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13-0CT-1999;
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                                                                                                                                                                                             FNNDADEEDFDGDDDGDEEGEEDDDDEEEED
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                                                                                                                                                                                                                                   KKGS-----KRALPEESFFTWFTDAQHKE-----DAGDEIHDEVADIIKEDLWSNPLTY 222
                                                                                                                                                                                                                                                                             l Similarity
26; Conserv
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990S-0158229

990S-0159229

990S-0159229

990S-0159239

990S-0159330

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990S-0159637

990S-0160741

990S-0160740

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990S-0160815

990S-0160880

990S-0160880

990S-0161405

990S-0161405

990S-0161405

990S-0161359

990S-0161351

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990S-0161353
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990S-0156458.
990S-0156596.
990S-0157117.
990S-0157753.
990S-0157865.
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99US-0154039.
99US-0154779.
99US-0155139.
99US-0155486.
                                                                                                                                                                                                                                                                                     12.5%;
                                                chromosome 2; human malaria parasite; vaccine;
protozoacide; infection; insecticide.
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Pred. No. 19;
12; Mismatches
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99US-0141287
99US-0141287
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99US-0151033

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                                                                                                                                                                                                                                                     AAB95086
                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                   Homo sapiens
                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                             Human protein sequence SEQ ID NO:16999.
                                                                                                                                                        26-JUN-2001
                                                                                                                                                                                                                                     AAB95086 standard;
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GARDNER
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27; Conserv
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                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                     Protein;
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Pred. No. 25;
9; Mismatches
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                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc golynucleotide which comprises a 5'-end cc golynucleotide comprises a 3'-end sequence complementary to a complementary to a complementary to a compount of the specification. The primer sets can be used in antisense therapy and compared the specification. The primers are useful for synthesising polynucleotides, can be used in antisense therapy and compared the compount of the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers also useful for the compared the compared that the proteins encoded by the full-useful condition and sequence is generally of the proteins encoded by the full-useful condition and sequences and and condition of the cDNAs easily without any specialised methods. AAH03166 to AAH13628 and condition conditions are present buman amino acid sequences; and AAH13629 to AAH13632 conditions.

Conditions of the present invention.
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02-MAY-2000;
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27-AUG-1999;
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EE-DED 281
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Search completed: May Job time : 59 secs

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Maximum DB seq length: 2000000000
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-258-287B-59
US-08-258-287B-57
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PCT-US94-07926-41
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; MOLECULE TYPE: US-08-044-547-3

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14.0%; Score 80.5; DB 32.7%; Pred. No. 0.21; 10;

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RESULT 1 US-08-044-547-: Sequence 3, 2 Patent No. 5: GENERAL INFO APPLICANT: APPLICANT: TITLE OF 1 TITLE OF 1 TITLE OF 2 TITLE OF 2 TITLE OF 3 TITLE OF 3 TITLE OF 1 TITLE OF 2 TOWNERS: STREET: COUNTRY: ZIP: COUNTRY: ZIP: COMPUTER F MEDIUM 1 COMPUTER F MEDIUM 7 COMPUTER F APPLICAL APPLICAL FILING I CLASSIP PRIOR APPLICAL FILING I TELEFAX: TELEFAX: TELEFAX: INFORMATION SEQUENCE C STRANDED TOPOLOGY MONTEL F TYPE: TYPE: STRANDED TOPOLOGY MONTEL F TYPE: TYPE: TOPOLOGY MONTEL F TYPE:	200 200 200 200 200 200 200 200 200 200
Sequence 3, Application US/06 patent No. 5324715 GENERAL INFORMATION: APPLICANT: Connolly, Thom APPLICANT: Connolly, Thom APPLICANT: Connolly, Thom APPLICANT: Keller, Paul Prote TITLE OF INVENTION: Colla APPLICANT: Keller, Paul TITLE OF INVENTION: Colla APPLICANT: Relear, Colla APPLICATION ET SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: P.O. BOX 2000 CITY: Rahway STATE: New Jersey COUNTRY: US ZIP: 07065 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy dis COMPUTER: IBM PC COMPATION COMPUTER: PATENTION DATA: APPLICATION NUMBER: US FILING DATE: US FILING DATE: US FILING DATE: 09-OCT-199 ATTORNEY/AGENT INFORMATION NAME: PATI, Richard S. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER: 32 REFERENCE	64. 64. 65. 66. 66. 66. 66. 66. 66. 66. 66. 66
Application US/(5324715 FORMATION: FORMATION: T: Keller, Paul TINVENTION: Prot INVENTION: Prot INVENTION: Paul TINVENTION: Paul TINVENTION: Prot INVENTION: Prot INVENTION: Prot INVENTION: Prot INVENTION: Prot INVENTION: Prot INVESTEM: PC-000 Rahway New Jersey Y: US TYPE: Floppy di ER: IBM PC-000 READABLE FORM: TYPE: IBM PC-Compa ING SYSTEM: PC-T REI PATON NUMBER: US DATE: US DA	11.3 111.3 111.3 111.0 111.0 111.0 111.0 111.0 110.9 110.9 110.9 110.9 110.9 110.9
aution US/080445 ON: ON: ON: ION: Protein f ION: Protein f ION: Protein f ION: Collagen- NCES: 12 ADDRESS: lerck & Co., Inc Box 2000 ersey LE FORM: Floppy disk Floppy disk Floppy disk PLOPDY disk PLOPOY disk PLOPOY disk PLOPOY disk PLOPOY disk PLOPOY disk NOWBER: US/08/0 N: 514 ON DATA: UMBER: US/08/0 N: 514 ON DATA: UMBER: 3,586 NUMBER: 3,586 NET NUMBER: 18 ON INFORMATION: NIFORMATION: 908) 594-4958 8) 594-4720 100 DATA: 110	1148 1148 11558 11726 11726 11726 11726 250 250 2557 21572 2177 2177 2177 2177 2177 217
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347 4. 6. Stimulated Platelet 1. 1. 1. 1. 2. 4. 3. 94,917 94,917	US-09-362-230-36 PCT-US94-07926-36 US-09-172-841-5 US-09-172-841-5 US-08-609-049A-13 US-08-609-049A-3 US-08-1609-059-3 US-09-170-996-3 US-09-134-996-5 US-09-293-273-5 US-09-293-273-5 US-09-293-273-5 US-09-293-273-3 US-08-702-153-4 US-09-211-930-3 US-09-340-993-3 US-09-468-442-3 ALIGNMENTS
Aggregation	Sequence 36, Appl Sequence 55, Appl Sequence 13, Appl Sequence 11, Appl Sequence 10, Appl Sequence 30, Appl Sequence 30, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 10, Appl Sequence 21, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl

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                                                                                                                                                                Sequence 2, Application US/08741134 Patent No. 5861498
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                         APPLICANT: APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4958
TELEFAX: (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                 APPLICANT: Fernandes-Alnemri, Teresa TITLE OF INVENTION: IMMUNOPHILIN FKB TITLE OF INVENTION: AND TITLE OF INVENTION: METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                   NUMBER OF SEQUENCES:
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STRANDEDNESS: unl
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                                                                                                                                                                                                                                                                                  66 DCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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r: P.O. Box 2000
Rahway
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Alnemri, Emad S.
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Collagen-Stimulated Platelet Aggregation
12
                                     METHODS OF USING THE SAME
                                                                      IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
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                                                                                                                                                                                                            Sequence 16, Application US/09187789

Patent No. 6340740

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
TITLE FILE REFERENCE: 480140.43401
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 167
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                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: Worldberfect for Windows 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 DE--NDESFKMN--TSAEGDDSDEEDDDDEDEEDEEDDD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 ANKKAKPDKKAGKNSAPAAESDSDDDD------EDQLQK-----FLDGEDIDT 174
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CITY: Philadelphia
STATE: Pennsylvania
44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. STREET: One Liberty Place - 46th floor
                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                            Conservative
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                                                                              13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 80.5; DB 30.6%; Pred. No. 0.87; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us 60/007,163
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                                                                                Score 75.5;
Pred. No. 1;
                                                                Mismatches
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                                                                                                   Length 172;
                                                              Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 480140.434
CURRENT APPLICATION NUMBER: US/09/139,600
CURRENT FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APC
TITLE OF INVENTION: AND METHOD OF USE
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                              APPLICATION NUMBER: US 08/08
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         APPLICATION NUMBER: US/08/258,287B FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                      Washington
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                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                 US 08/080,850
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                    0609.3920001
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US-08-368-704C-56
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Best Local :
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
                                                                                                                    INFORMATION FOR SEQ ID NO:
              TOPOLOGY: u
                                                                                                                                                               REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 06i
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,704C
                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: pept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
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                                                                                                                             TELEPHONE: (202) 371
TELEFAX: (202) 371
TELEX: 248636 SSK
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600
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STRANDEDNESS: unl
                                                                                  CENGTH:
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                                                              amino acid
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                                                                              418 amino acids
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                                                                                                                                                                                                        0609.3920002
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Pred. No. 3;
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US-08-368-704C-55
              RESULT 9
                                                                                                                                                                                                                                                                           US-08-258-287B-57
                                                                                                                                                                                                                        Query Match 13.2%;
Best Local Similarity 35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 57, Application US/08258287B Patent No. 6083735
                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bugaiský, Lawrence B.
REGISTARTION NUMBER: 35,086
REFERENCE,DOCKET NUMBER: 06.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Programmed Cell Death Genes and Proteins NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
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                                                                 82 EQLSLQFSNDEDD 94
                                                                                                  95 DE-----SDEVD 101
                                                                                                                                    26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                   44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                          LENGTH:
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STREET: 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                         26;
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                                                                                                                                                                                                                                                                                                                                          419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              : (202) 371-2600
(202) 371-2540
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/258,287B
10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 75.5; 35.6%; Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0609.3920001
                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                          Score 75.5;
Pred. No. 3;
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; MOLECULE TYPE: protein
US-08-368-704C-55
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US-08-170-360-1
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                                                                                                                                                                                Sequence 1, Application US/08170360 Patent No. 5656602
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                  GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLAZ INHIBITORY COMPOUNDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0609.3920002 TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US,
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yuan, Junying APPLICANT: Miura, Masayuki
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TELEFAX: (202) 371
TELEX: 248636 SSK
                               STREET:
                                                                                                                                                                                                                                                                                                                                   95 DE-----SDEVD 101
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                                                                                                                                                                                                                                                                                                                                                                                                          44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bugaisky, Lawrence B. REGISTRATION NUMBER: 35,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 10-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                82 EQLSLQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 419 amino acids
TYPE: amino acid
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STATE:
                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
1 Similarity 35.6%;
26; Conservative 1
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Washington D. C.
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                                 E: Rothwell, Figg Ernst & Kurz
Suite 701-E, 555 Thirteenth St.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
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Pred. No. 3;
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COMPUTER READABLE FORM:

COUNTRY: U.S.A.

20004

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RESULT 11
US-08-961-083-200
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 200, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 16;
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Choi et. al. TITLE OF INVENTION: Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-JUL-
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                                                                CLASSIFICATION: 435
                                                                                 FILING DATE:
                                                                                            APPLICATION NUMBER: US/08/961,083
                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                        CITY: Rockville
                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                        ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                           Maryland
                                                                                                                                                                                                                                                                      9410 Key West Avenue
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(202)783-6031
(202)783-6031
                                                                                                                                                                                                                           USA
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                                                                                                                                                            HP Vectra 486/33
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27.1%;
                                                                                                                                           MSDOS version 6.2
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                                                                                                                                                                       3.50 inch, 1.4Mb storage
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RESULT 12
US-08-170-360-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARENT NO. JOYANATION:
BAPPLICANT: Tseng, Albert P. S.
BAPPLICANT: Toglis, Adam
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
TITLE OF SPOURNCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08170360 Patent No. 5656602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                 TELEFAX: (202)783-603 INFORMATION FOR SEQ ID NO:
                                                              SEQUENCE CHARACTERISTICS LENGTH: 124 amino acic
                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (202)783-6040
                                                                                                                                                                                                              FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
MOLECULE TYPE:
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polarian
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                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite 70 CITY: Washington STATE: D. C.
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                TELEPHONE:
                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                  NAME: Ernst, Barbara G. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ELDQEKF-----VVDENFTENYLTDCEG-----KDAGNAAGTGDE 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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V. U.S.A.
                                                amino acid
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Suite 701-E, 555 Thirteenth St., N.W
                                                           124 amino acids
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                                                                                                               (202)783-6031
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protein
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Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
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Query Match
Best Local Similarity
Watches 17; Conserve
Q
                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-888-497-41
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US-08-888-497-41
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                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41, Application US/08888497 Patent No. 5972677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 00 FILING DATE: 26-JUL-1993 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 200 buccale
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   27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                               NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 33301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Ruden, Barr
ADDRESSEE: Russell PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 SGNVITCSDKNNDCE 92
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                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                     124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                             305-764-4996
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                                      Conservative
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                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; Score 67; DB 1; Length 124; 22.7%; Pred. No. 5.4; tive 14; Mismatches 22; Indels
                                                    11.7%; 22.7%;
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                                      14;
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                                                    Score 67; D
Pred. No. 5.
                                      Mismatches
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                                                                     DB 2;
                                      22;
                                                                       Length 124
                                      Indels
                                      22;
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US-09-362-230-41
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 305-764-4996 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Fort Lauderdale
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  78
                                       87 AGNAAGTGDESDEVD 101
                                                                              40 DLDRC---CQTHDHCY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/097,354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                        Local Similarity es 17; Conserv
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SGNVITCSDKNNDCE 92
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                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                          Conservative
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                                                                                                                                                                             11.7%; Score 67; DB 4; Length 124; 22.7%; Pred. No. 5.4;
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                                                                                                                                                            Mismatches
                                                                              ---NQAKKLESCKFLIDNPYTNTYSYKC----
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                                                                                                                                                          22;
                                                                                                                                                            Indels
                                                                                                                                                               22;
                                                                                                                                                            Gaps
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RESULT 15 PCT-US94-07926-41

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; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 4
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07926-41
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Search completed: May 5, 2003, 17:51:12 Job time: 23 secs
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ZIP: 3301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEY,ACENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 305-527-2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                         78 SGNVITCSDKNNDCE 92
                                                                                                                                                              87 AGNAAGTGDESDEVD 101
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                                                                                                                                                                                                                                                         27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard CITY: Fort Lauderdale STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 amino acids
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
              Query
Match
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573
1 EEREDCWTFYANRKY
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//cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
//cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
//cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
//cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
//cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
//cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
//cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
//cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *
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//cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep: *
//cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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          172
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10 US-09-989-903-16

10 US-09-833-790-252

10 US-09-815-242-11522

10 US-09-765-272-200

10 US-09-993-999-7
                                          US-09-953-280-46
US-09-801-574-57
US-09-80-748-11327
US-09-974-298-114
US-09-975-4568-5
US-09-975-4568-5
US-09-075-4568-5
US-010-806-695
US-10-102-806-695
US-10-042-477-52
US-10-042-477-52
US-10-042-477-52
US-10-042-477-52
US-10-042-477-52
US-10-042-477-52
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US-10-042-477-52
US-10-042-477-52
          US-09-930-871-18
US-09-930-871-20
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253.929 Million cell updates/sec
Sequence 16, Appl
Sequence 15, Appl
Sequence 252, App
Sequence 200, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 57, Appl
Sequence 114, Appl
Sequence 511, App
Sequence 511, App
Sequence 52, Appli
Sequence 52, Appli
Sequence 52, Appli
Sequence 53, Appli
Sequence 54, Appli
Sequence 10, Appli
Sequence 10, Appli
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61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	63	63	63	63	63	63
10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	11.0	11.0	11.0	11.0	11.0	11.0
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US-10-125-852-25	US-09-894-912A-13	US-09-894-912A-34	US-09-894-912A-10	US-10-125-852-23	US-09-816-028A-39	US-09-894-912A-26	US-09-894-912A-16	US-10-185-770-4	US-09-867-550-2038	US-10-118-513A-12	US-10-118-513A-8	US-10-118-513A-2	US-09-822-682-2	US-09-919-770-4	US-10-060-036-171	US-09-919-603-2	US-09-821-839-2	US-09-925-301-1031	US-09-872-523-3	US-09-930-871-12	US-09-930-871-2	US-09-930-871-14	US-09-930-871-4	us-09-930-871-16	US-09-930-871-6
25,	13,	34,	10,	3	m	26,	16	App	e 20	12,	8	Sequence 2, Appli	ν,	Sequence 4, Appli	171,	ν ,		Sequence 1031, Ap	ω ~	12,	2,	14	4, 2	16,	Sequence 6, Appli

ALIGNMENTS

RESULT 1 US-10-068-564-16

Sequence 16, Application US/10068564
Publication NO. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
TITLE OF INVENTION: AND METHODS OF USE
FILLE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 16 LENGTH: 172

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; Sequence 16, Application US/09989903
; Patent NO. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                           RESULT 2
US-09-989-903-16
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-068-564-16
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Matches
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                                                                                                                                                       US-09-815-242-11522
; Sequence 11522, Application US/09815242
; Patent No. US20020061569A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 252
LENGTH: 156
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APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
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CURRENT APPLICATION NUMBER: US/09/989,903
CURRENT FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lodes, Michael J. APPLICANT: Wang, Tongtong
                                                                             APPLICANT:
                                                                                                  APPLICANT:
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                                          APPLICANT:
                                                           APPLICANT:
    APPLICANT:
                      APPLICANT:
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Local Similarity 35.6%;
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                                                                                                                                                                                                                                                                                                                45 FEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
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                                                                                                                                                                                                                                                                                                                                                                                            1 EERE-----DCWTFYANRKYTDFDKS----FKKSSD------LDECKKTCFKTEYCYIV 44
                                                                                                                                                                                                                                                                           YYSRADAENAMRYINGTRLDDR--IIRTDWDAGFK---EGRQYGRGRSGGQVRDEYRQD 141
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Secrist, Heather
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Indirias, Carol Y.
Yamamoto,
                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                  Carr, Grant J.
                                        Trawick, John D.
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    Robert T
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US-09-815-242-11522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11522
LENGTH: 1167
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 DKTEQSSNDPKEAQKTLFDA----ILLQDLAN--AVYNVMPTK------LGDRNYWENF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENY 78
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                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                           APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
FILING DATE: <Unknown>
ATTORNBY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REGISTRATION OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452\,
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi et. al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: HP Vectra 400/55
OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
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                                                   REFERENCE/DOCKET NUMBER: PB340P2
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-993-999-7
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                                                                                                                                                                                                Sequence 46, Application US/09953280 Publication No. US20030073072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09993999 Patent No. US20020110891A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                        APPLICANT: Havenga, Menzo
APPLICANT: Vogels, Ronald
APPLICANT: Bout, Abraham
TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
EILE REFERENCE: 2183-4123US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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                CURRENT APPLICATION NUMBER: US/09/953,280 CURRENT FILING DATE: 2001-09-14 PRIOR APPLICATION NUMBER: US 09/348,354 PRIOR FILING DATE: 1999-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Austen, K. Frank
APPLICANT: Glimcher, Laurie H.
TITLE OF INVENTION: Phospholipase A2 Group Preferentially
TITLE OF INVENTION: Expressed in Th2 Cells
FILE REFERENCE: HUI-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/246,316
PRIOR FILING DATE: 2000-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/993,999 CURRENT FILING DATE: 2001-11-06
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 WIKQLNKRLEKFD-----SEIINCRVTSEQISCYKSDISYTVF-----LRYFIADFV 368
                                                                                                                                                                                                                                                                                                                                   62 DLDRC---CQTHDHCY------SQAKKLESCKFLIDNPYTNTYSYSCSGSE 103
                                                                                                                                                                                                                                                                                                                                                                        27 DLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ELDQEKF-----VVDENFTENYLTDCEG-----KDAGNAAGTGDE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 11.9%;
Local Similarity 25.0%;
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STRANDEDNESS: single
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(301) 309-8512
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23.6%; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                      9,
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                      Sequence 1327, Application US/09880748 Publication No. US20030059937A1
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/09801574 Patent No. US20020081592A1
                                                                                                                                                                                          APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: pF523
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Best Local Similarity
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                                                                                                     CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                              PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
                    PRIOR APPLICATION NUMBER: 60/276,248 PRIOR FILING DATE: 2001-03-16
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR APPLICATION NUMBER: 60/261,557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Reproduction-Specific Genes FILE REFERENCE: 0399.2007-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Peijing Jeremy APPLICANT: Page, David C.
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TYPE: PRT
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APPLICATION NUMBER: 60/277,379
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Pred. No. 72;
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US-09-974-298-114
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APPLICANT: Chen, Huei-Mei
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
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SEQ ID NO 1327
LENGTH: 257
                                                                                                                                                                       GENERAL INFORMATION:
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SEQ ID NO 114
LENGTH: 1125
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PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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                                                                                                      APPLICANT: LAZDUNSKI, MICHEL APPLICANT: LAMBEAU, GERARD APPLICANT: VALENTIN, EMMANUEL
                    CURRENT APPLICATION NUMBER: US/09/975,456B CURRENT FILING DATE: 2002-08-27
                                                              TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2 FILE REFERENCE: 1478-R-00
PRIOR APPLICATION NUMBER:
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OTHER INFORMATION: Incyte ID No. US20020156263A1 3267030CD1
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                                                                                                                                                                                                                                                                                                                      1076 EEVEEAENEGEEAKTEGLMKDDRAESQASSLGQKVGESSEQVSEE 1120
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nes 24; Conserv
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    60/239,491
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Pred. No.
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39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 1125;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SITE ; LOCATION: (156) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-297-511
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US-10-102-806-695
SOFTWARE: Pat
SEQ ID NO 695
LENGTH: 460
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    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

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Best Local
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                                                     PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                           APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA103PIC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925/298

PRIOR FILING DATE: 2001-08-10

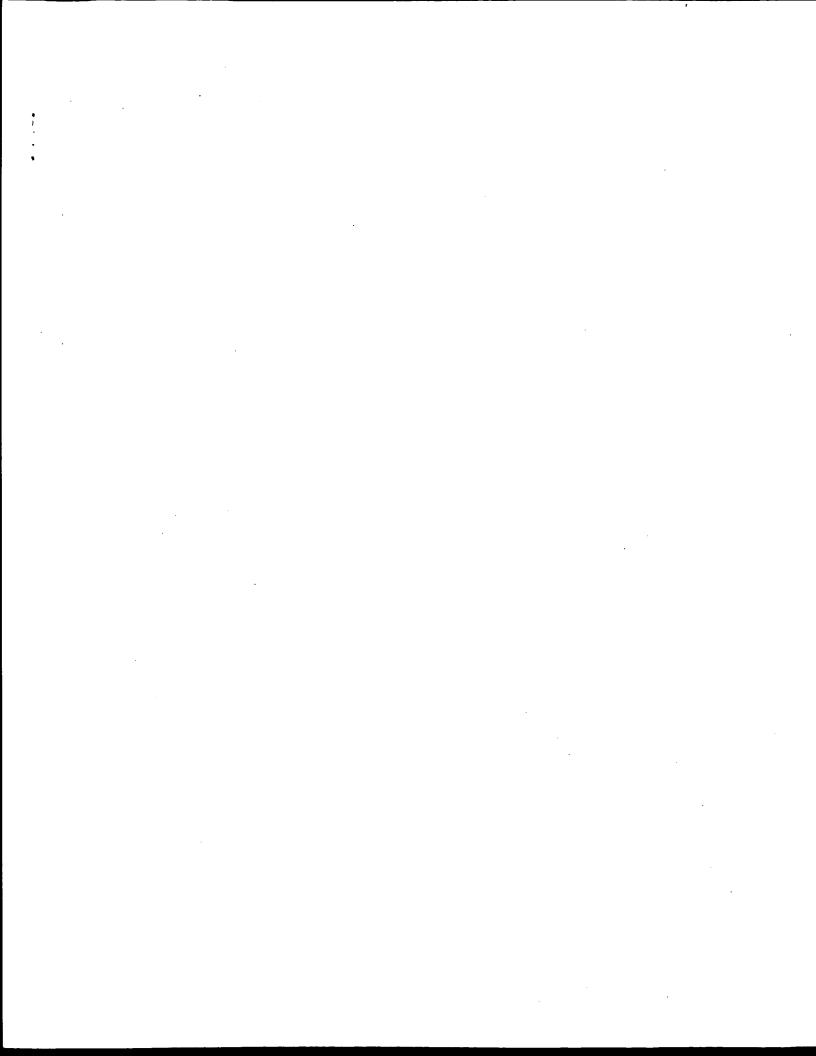
PRIOR FILING DATE: 2001-08-10
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
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Local Similarity 29.8%;
es 17; Conservation
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                                        PatentIn Ver.
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29.8%;
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Pred. No. 18;
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Pred. No. 19;
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RESULT 15
US-10-092-219-8
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; LICATION: all Xaa positions
; OTHER INFORMATION: Xaa-unknown amino acid residue
US-10-042-417-52
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
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                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Domin, Jan
                                                                                                                                                                                                                                                         Sequence 8, Application US/10092219
Patent No. US20020115114A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.2%; Score 64; DB Best Local Similarity 27.1%; Pred. No. 96; Matches 23; Conservative 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/10042417 Patent No. US20020123082A1
TITLE OF INVENTION: No. US20020115114A1e1 Lipid Kinase FILE REFERENCE: 1064Hg/50947 CURRENT APPLICATION NUMBER: US/10/092,219 CURRENT FILING DATE: 2002-03-07 PRIOR APPLICATION NUMBER: PCT/GB98/00244 PRIOR PILING DATE: 1998-01-27 PRIOR PILING DATE: 1998-01-27 PRIOR APPLICATION NUMBER: PCT/GB98/00244 PRIOR PILING DATE: 1998-01-27 PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999
CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVD---GEELDQE----KF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 VDGEELDQE---KEVVDENFTENYLTD----CEGKDAGNAA---GTG-----
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Search completed: May Job time : 36 secs
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 9701652.1
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 294
                                                                                                                                                                                                            Query Match 11.0
Best Local Similarity 28.8
Matches 19; Conservative
                                                                      104 LLDDNF 109
                                                                                                         69 VYDENF 74
                                                                                                                                          45 DRQMTDSPRGFELSSSTRQRTQGFNKQDYDLMVFPELDSQKRAVD-IDVEKLTQAELEKI 103
                                                                                                                                                                         12 NRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ---EKF 68
                5, 2003, 17:54:15
                                                                                                                                                                                                           11.0%; Score 63; DB 28.8%; Pred. No. 55; tive 18; Mismatches
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55;
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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd
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OM protein - protein search, using sw model

Run on: мау 5, 2003, 17:48:57; Search time 36 Seconds

(without alignments)
275.051 Million cell updates/sec

Title:

Perfect score: US-09-936-737A-2 573 1 EEREDCWTFYANRK

EEREDCWTFYANRKYTDFDK......GKDAGNAAGTGDESDEVDED 103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

Database : PIR_73:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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68.5	68.5	69	69	69	69	69.5	69.5	69.5	69.5	69.5	70	70	70	70	70.5	
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D70100	T26487	T18444	T28317	T33328	T32824	AI3625	D95206	S61160	T37899	PSPGA	В97104	F71909	S50295	T24432	C86406	
phosphoglucomutase	hypothetical prote	hypothetical prote	ORF MSV156 hypothe	hypothetical prote	hypothetical prote	ribonucleoside-dip	hypothetical prote	hypothetical prote	hypothetical prote	phospholipase A2 (hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	88.6K hypothetical	

ALIGNMENTS

A42435

leech antiplatelet protein precursor - Mexican leech C;Species: Haementeria officinalis (Mexican leech) C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-May-1999 C;Accession: A42435; A42434

R;Keller, P.M.; Schultz, L.D.; Condra, C.; Karczewski, J.; Connolly, T.M. J. Biol. Chem. 267, 6899-6904, 1992
A;Title: An inhibitor of collagen-stimulated platelet activation from the salivary gla;Reference number: A42435; MUID:92202247; PMID:1551898
A;Accession: A42435...

A; Molecule type: mRNA A; Residues: 1-147 <KEL>

for residu

A; Cross references: GB:M81489
A; Note: the authors translated the codon AGC for residue 20 as Arg and GAA:
A; Note: the authors' translation is shown at residue 65
A; Note: sequence extracted from NCBI backbone (NCBIN:91615) and modified
R; Connolly, T.M.; Jacobs, J.W.; Condra, C.
J. Biol. Chem. 267, 6893-6898, 1992
A; Title: An inhibitor of collagen-stimulated platelet activation from the standard collagen and the standard platelet activation from the standard collagen. A42434; MUID:92202246; PMID:1551897
A; Accession: A42434 salivary gl

A; Molecule type: protein A; Residues: 59-91; 101-113; 123-139 <CON>

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-147/Product: leech antiplatelet protein #status predicted <MAT>

Query Match Match 14.0%; Score 80.5; DB 2; Local Similarity 32.7%; Pred. No. 1.7; Conservative 10; Mismatches 24; Length 147; Indels **υ** Gaps

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B QУ 66 DCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRN 120 5 DCWTFYANRKYTDFDKSFKKSSDLDECKKTCFKTEY---CYIVFEDTVNKECYYN 56

RESULT 2 A55320

immunophilin FKBP46 - fall armyworm
C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 02-Sep-2000
C;Accession: A55320

R;Alnemri, E.S.; Fernandes-Alnemri, T.; Pomerenke, K.; Robertson, N.M.; Dudley, K.; D J. Biol. Chem. 269, 30828-30834, 1994
A;Tille: FKBP46, a novel 5f9 insect cell nuclear immunophilin that forms a protein-kia;Reference number: A55320; MUID:95074110; PMID:7527037

A; Reference number: A55320; A; Accession: A55320

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-412 <ALN>

A;Cross-references: GB:U15038; NID:g595844; PID:g595845 C;Superfamily: yeast peptidylprolyl isomerase FPR3; BKBP-type peptidylprolyl isomeras

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hypothetical protein Y69H2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A:Introns: 23/3; 65/1; 105/1; 146/1; 191/1; 241/1; 293/1; 381/1; 419/1; 461/1; 499/1; 55
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26562
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F;324-371/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-907 <WIL>
A;Cross references: EMBL:Z98877; PIDN:CAB11570.1; GSPDB:GN00023; CESP:Y69H2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 134/3; 160/1;
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A;Experimental source: clone Y26D4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 220234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T26562
                                                                                                                                              A; Gene: CESP:Y69H2.2
                                                                                                                                                                                     A; Experimental source: clone Y69H2
                                                                                                                                                                                                                                                                            A; Reference number: Z20343
A; Accession: T27317
                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:Y26D4A.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 CGNFLHNRPYPDSCETECMDTMVQVNAKPGPLMGSRNIKDNLTSSDECVKYCWKDLNCFV 229
 10 YANRKYTDFDKSFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 VFEDTVNKECYYNVVDGEELDQEKFVVDEN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED 103
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                                    33; Conser
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30.6%;
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                                                      13.7%;
29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches 29;
 ---KSSDL-----DECKKTC--FKTEYGYIVFEDT
                                      12; Mismatches
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                                                      Score 78.5; DB Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DKSFKKS-SDLDECKKTCFKTEYCYI 43
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A; Residues: 1-797 < ALB>
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A; Residues: 1-682 <STO>
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                 382 ANEK--EYKKIIDKSDDRDDRDKDEYELE-----
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                                                                                                          13.6%;
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J. Virol. 66, 5047-5058, 1992
A;Title: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A37309; MUID:92333688; PMID:1321287
A;Contents: annotation; protein-coding frames
A;Note: neither protein nor nucleotide sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45671.1; PID:g60369 R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, J. Virol. 66, 5047-5058, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus
A;Reference number: A36806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: chemotaxis protein cheA
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                two-component sensor histidine kinase involved in chemotaxis cheA [imported] - Bacill C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ORF48 - saimiriine herpesvirus 1 (strain 11)
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11 ANRKYTDFDKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYN----VVDGEELDQE 66
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                                                                                                         Score 78;
Pred. No.
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RESULT 8
T16354
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A;Description: The sequence of C. elegans cosmid F4:
A;Reference number: Z18498
A;Accession: T16354
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F42G9.1 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16334 R;Taich, A.
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A;Introns: 37/3; 254/2; 364/2; 406/2
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A; Cross-references: EMBL:U00051; NID:g1216305;
A; Experimental source: strain Bristol N2
C; Genetics:
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A;Cross-references: EMBL;Z77661; PIDN:CAB01183.1; GSPDB:GN00023; CESP:F40G12.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
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                                                                                                             10 YANRKYTDF--DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEK 67
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                                   FVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD 101
   DIGDEG --
                                                                         FTSAKLPDFLKERKFWEADDVAECLQKAF-----VDFDDFIRAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFLEIVK-EECPEEKFKLIEENYSQLVTLLTE-KPKDNGACTAPYFQLEEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYYNVVDGEELDQEKF-VVDENFTE--NYLTDCEGKDAGNAAGTGDESDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEKEEGEDEGDDGEDEGEDEGE--DEGDEGDE 461
                                                                                                                                                      23;
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                                                                                                                                                                        Similarity
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                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
-KPKKAGGEADSEDEADRID 137
                                                                                                                                                                      13.2%;
24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%; 27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FEKVFLAIISGKHECSK-----DYDFLARNLIQRREALTSGKE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                    18; Mismatches
                                                                                                                                                                        Score 75.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                    elegans cosmid F42G9.
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                                                                                                                                                                                                                                                                                                     PID:g1216310;
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                                                                                                                                                                                                                                                                                                 PIDN:AAA91358.1; CESP:F42G9
                                                                         ESMKELK 112
                                                                                                                                                25;
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PAR interacting protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                   B
R;Comte, P.A.; Ossipow, V.; Schibler, U. submitted to the EMBL Data Library, January 1997
                                                     C; Accession: T32731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
A;Introns: 23/1; 48/1; 158/3; 216/1; 264/1; 312/1; 331/3
C;Superfamily: Caenorhabditis elegans hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: aarpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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A; Residues: 1-3844 <B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Barale, J.C.; Candelle, D.; Attal-Bonnefoy, G.; Dehoux, P.; Bonnefoy, S.; Ridley, R Infect. Immun. 65, 3003-3010, 1997
A;Title: Plasmodium falciparum AARP1, a giant protein containing repeated motifs rich A;Reference number: Z18929; MUID:97378065; PMID:9234746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-360 <TAI>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z21535
A; Accession: T34510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ZK1290.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000 C;Accession: T34510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                   1786 K-KKNKKNVENQEKEFYVLNKIFVHNFI 1812
                                                                                                                                                                                                                                                                                                                                                1726 EDSEECQIKESYKKMSECNNKENIIFDSISVLRKNNIKRLKNYMCKNKNCYIYYDDNNNK 1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 EDTVGEE----NVFDFDKLFDKKIYIRNDGSTTENTTEQSTTEKTGTKKGTIEVSVELGEG
                                                                                                                                                                                                                                                                                                52 ECYYNVVDGEELDQEKFVVDENFTENYL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 DESDEVDED 103
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23.9%;
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
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A; Gene:
C; Superf
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A;Reference number: Z21213
A;Accession: T32731
A;Status: preliminary; translated
                                                                              Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID:98065943; PMID:9403885
A; Accession: B70236
                                                                                                                                                                                                                                                       hypothetical protein BBH09 - Lyme disease spirochete plasmid H/lp28-3 c;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999 c;Accession: B70336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: D70465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein aq_1923 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May_1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70465
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A;Cross-references: EMBL:U83590; NID:g2253210; PID:g2253211; PIDN:AAB62878
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A; Residues: 1-1277 <COM>
                                         A; Molecule type: DNA
                                                                                                                                                                                                              son,
                                                                                                                                                                                                                             R; Fraser,
                                                                                                                                                                                                                                                   C; Accession: B702
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A; Residues: 1-296 < AQF>
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                   A; Residues:
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                                                           A; Status: preliminary; nucleic acid sequence not shown;
Cross-references: GB:AE000784;
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Best Local :
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                                                                                                                                                                aser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
wman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
re 390, 580-586, 1997
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                        1-1278 <KLE>
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30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%; Score 74; DB 24.2%; Pred. No. 14;
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    NID: g2690041;
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Pred. No. 53;
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    PIDN:AAC66000.1; PID:g2690056; TIGR:BBH09
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hypothetical protein F26F2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Caccession: T21428 R;Ainscough, R. Submitted to the EMBL Data Library, November 1996
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A; Residues: 1-4466 < OGA>
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                                                                 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A, Molecule type: mRNA
A, Residues: 764-1001, 'App', 1005-2036, 'VPSSVET' <0G2>
C, Superfamily: dynein heavy chain, ciliary
C, Keywords: ATP; heterotetramer; hydrolase; microtubule
F, 154-161/Region: nucleotide-binding motif A (P-loop)
F, 1852-1859/Region: nucleotide-binding motif A (P-loop)
F, 2133-2140/Region: nucleotide-binding motif A (P-loop)
F, 2460-2467/Region: nucleotide-binding motif A (P-loop)
F, 2805-2812/Region: nucleotide-binding motif A (P-loop)
F, 160/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dynein beta heavy chain, ciliary - sea urchin (Anthocidaris N;Contains: dynein ATPase (EC 3.6.4.2) C:Species: Anthocidaris crassispina C:Species: 30-Sep-1991 #sequence_revision 02-May-1994 #text_chac;Accession: S17231; PS0415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 352, 643-645, 1991
A;TitLe: Four ATP-binding sites in the midregion of the beta heavy chain of dynein.
A;Reference number: S17231; MUID:91326104; PMID:1830928
A;Accession: S17231
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A; Accession: PS0415
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FKMLDCYGPLLDRPVIRNDF---ECKYPIVLMLYDQELDQSKEIYDEH
                                                    FKTEYCY-----IVFEDTVNKECYYNVV---DGEELDQEKFVVDEN 73
                                                                                                            EEFQECAKVFTERPYDGLDPTCQEFLEDYEEFEKKVFDLDRRLGSILCQGFDDCCGLEAA 519
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Pred. No. 59;
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Pred. No. 2.1e
14; Mismatches
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PA21_PIG
CALG_HUMAN
CC45_YEAST
MOK1_SCHPO
MOK2_CANPO
FABL_ANOPU
PA21_HORSE
LHX1_BRARE
CALX_RAT
YJQ8_YEAST
                                                                 PA21_MOUSE
NEF_HV2D2
DYHC_TRIGR
PS12_ARATH
D7_AEDAE
SPT8_YEAST
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Compugen Ltd.
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Q26486 spodoptera
Q01033 herpesvirus
Q08736 mus musculu
P49595 caenorhabdi
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Q58285
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canis famil
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         rattus norv
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AC Q26486;
DT 01-NOV-1997 (
DT 01-NOV-1997 (
DT 15-JUL-1999 (

STANDARD;

PRT;

412 AA

(Rel. (Rel. (Rel.

35, Created)
35, Last sequence update)
38, Last annotation update)

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33: vative DFDKSF : DNLLTK	AAA29194.1; 1 21 1 147 AA; 15908	OT entry is copy Swiss Institute Bioinformatics I profit institut this statement I this statement I license I	ression."; 17:6899-6904(INHIBITOR OF DENSE GRANUL OCATION: Sec	.A., AND SEQUENCE gland; gland; 7; PubMed=1551898 hultz L.D., Condr f collagen-stimul of the Haementer	alis Anne ossip		STANDARD;		1033 1448 1647 1657 1728 428 455 725 746 793 1124 1281
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al Similarity 33.9%; pred. No. 0.2; al Similarity 33.9%; pred. No. 0.2; 19; Conservative 10; Mismatches 24; Indels 3 19; Conservative 10; Mismatches 24; Ind	POTENTIAL. ANTI-PLATBLET PROTEI; 75A5511374A4E42E C	pyright. It is p e of Bioinformat Institute. The utions as long is not removed. agreement (See @isb-sib.ch).	EN-STIMULATED	OF 60-91 AND Karczew Compared platelet Compared	leech). tellata; Hiru Haementeria.	Created) Last sequence update) Last annotation update) precursor.	PRT; 147 AA.	ALIGNMENTS	S190_YEAST CB20_XENLA YDE1_SCHPO ADF1_CAEEL RF4_KLULA YNU6_YEAST RIF1_MYCTU GYP7_YEAST NETB_DROME TCF8_HUMAN TRPS_HUMAN VIT1_CAEEL
24; Indels 3; Gaps 1; CYIVFEDTVNKECYN 56 : CYILQINTETNECYRN 120		rough a collaboration he EMBL outstation restrictions on it tent is in no way and for commerciarisb-sib.ch/announce	TELET RELEASE	123-139. ski J., Connolly T.M.; activation from the sleech. II. Cloning of	Hirudinea;				P36123 saccharomyc P52299 xenopus lae Q10435 schizosacch Q07750 caenorhabdi P09806 kluyveromyc P50640 mycobacteri P40161 saccharomyc P50640 mycobacteri Q44568 drosophila P37275 homo sapien P37275 homo sapien Q9uhf7 homo sapien P55155 caenorhabdi

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Gammaherpesvirinae;
NCBI_TaxID=10383;
                                                                      Herpesvirus saimiri (strain 11)
                                                                                                                        Hypothetical gene
                                              Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                     VG48_HSVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase complex.";

J. Biol. Chem. 269:30828-30834 (1994).

-I- FUNCTION: BINDS TO, AND IS INHIBITED BY FK506 AND RAPAMYCIN. BIND DOUBLE-STRANDED DNA IN VITRO. PPLASES ACCELERATE PROTEIN FOLDING.

-I- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.

-I- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; G
Ditrysia; Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00454; FKBP_PPIASE_2; PROSITE; PS50059; FKBP_PPIASE_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U15038; AAA58962.1; -. HSSP; P20071; 1FKJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00254; FKBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "FKBP46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alnemri E.S., Fernandes-Alnemri T., Pomerenke K., Robertson N.M., Dubley K., Dubois G.C., Litwack G.;
                                                                                                                                                                                                                                                                                                                                                                                  175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 ANKKAKPDKKAGKNSAPAAESDSDDDD------EDQLQK-----FLDGEDIDT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95074110; PubMed=7527037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 kDa FK506-binding nuclear protein (Peptidyl-prolyl cis-transisomerase) (PPiase) (EC 5.2.1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 ANRKYTDFDKSFKKS-----SDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                         66 EKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                     OR EDLF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        DE--NDESFKMN--TSAEGDDSDEEDDDDEDEEDEEDDD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATED BY A NUCLEAR KINASE IN THE PRESENCE OF MG2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a novel Sf9 insect cell nuclear immunophilin that forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001179; FKBP_PPIase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
120
152
219
219
324
412 AA;
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                                                                                                                                                  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                        25, Created)
25, Last sequence update)
25, Last annotation updat
48 protein.
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216
302
                    Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear
                                            no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80.5; D
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; DNA-binding; Phosphorylation.
ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYS-RICH (BASIC).
PPIASE, FKBP-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYS-RICH (BASIC)
ASP/GLU-RICH (HI
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F2A69159AEF4FE22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                  797
                                              Herpesviridae
                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glossata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hexapoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                     RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY).

-- SUBUNIT: HETERODIMER OF TWO SUBUNITS (POTENTIAL).

-- TISSUE SPECIFICITY: MAINLY EXPRESSED IN SKELETAL MUSCLE AND LUNG.

-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                            "Characterization of seven murine caspase family members.";
FEBS Lett. 403:61-69(1997).
-I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           008736;
01-NOV-1997
                                                                                                                                                                                                                                                                                                  MEDLINE=97190206; PubMed=9038361; van de Craen M., Vandenabeele P., van Loo G., Molemans F., Schotte I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-12 precursor (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                       Fiers W.;
                                                                                                                                                                                                                                                                                                                                                           STRAIN=C3H/An;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64346; CAA45671.1; ~. PIR; A36811; A36811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary structure of the herpesvirus saimiri genome."; J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newman C., Wittmann Honess R.W.;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382
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41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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P., van Criekinge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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                                                                                                                                                                                                                                                                                                                    den Brande
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mus.
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RESULT
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Best Local Similarity
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                    the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
ACT_SITE
ACT_SITE
SEQUENCE
EMBL; U00051; AAA91358.1;
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                          Taich A., Waterston R.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                           STRAIN-Bristol N2;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                             F42G9.1
                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable protein phosphatase 2C F42G9.1 (EC 3.1.3.16) (PP2C).
                                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
CHAIN
                                                                                                                                 Phosphate.
-!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                 P49595;
                                                                                                                                                                                                                                                                                                                                                                                                              P2C1_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50209; CARD; 1.
PROSITE; PS01121; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00114; CARD; 1.
SMART; SM00115; CASC; 1.
                                                                                                                                                                            -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Thiol protease; Apoptosis; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002398; ICE_p10.
InterPro; IPR002138; ICE_p20.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; C14.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P29466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y13090; CAA73532.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 EQLSIQFSNDEDD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 VFEDTVNKECYYNVVDGEEL----DQEKFVVD--ENFTENYL--TDCEGK-DAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 DE----SDEVD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 VFDDLVEK----NVLNGDELLKIGESASFILNKAENLVENFLEKTDMAGKIFAGHIANSQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Casp12
                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%;
35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASPASE-12 SUBUNIT 2. CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASPASE-12 SUBUNIT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                           491 AA
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Best Local S
Matches 23
                                                                                                                    Matches
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                         smART; SM00254; ShKT; 1
Hypothetical protein; Signal.
SIGNAL
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METAL 37 37
METAL 38 38
METAL 57 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last ann
Hypothetical 39.7 kDa protein
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                              WormPep; ZK1290.10; CE02080.
InterPro; IPR003582; ShKT.
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U21308; AAB93316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadore: Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YOFA_CAEEL
Q09337;
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InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
Pfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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SMART; SM00332; PP2CC; 1.
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224 EDTYGEE----NVFDFDKLFDKKIYIRNDGSTTENTTEQSTTEKTGTKKGTIEVSVELGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 DIGDEG------KPKKAGGEADSEDEADRID 137
                                                    46 EDTVNKECYYNVVDGEELDQEKFVV-----DENFTENYLTDCEGKDAGN-----AAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 YANRKYTDF--DKSFKKSSDLDECKKTCFKTEYCYIVFEDTVNKECYYNVVDGEELDQEK 67
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                                                                                                                                               Similarity
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Lical protein; Hydrolase; Magnesium; Manganese.

37 37 MANGANESE 1 (BY SIMILARIT
                                                                                                                                                                                                                              360 AA;
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                                                                                                                                                                                                                              39669 MW;
                                                                                                                                            13.1%;
33.3%;
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Last annotation update)
protein ZK1290.10 in ch
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                                                                                                            Score 75; DB 1; Length 360
Pred. No. 4.8;
9; Mismatches 23; Indels
                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN ZK1290.10; 18751B6BC062D4F7 CRC64;
                                                                                                                                                                                                                                                                                  POTENTIAL.
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MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
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RESULT 8
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Best Local
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16-0CT-2001
                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-AAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, ciliary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hypothetical protein AQ_1923 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                    Anthocidaris crassispina (Sea urchin)
Eukaryota; Metazoa; Echinodermata; Ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Signal; Complete proteome. SIGNAL 1 20 POTENTIAL.
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                                                                                                                                                                              Echinoidea;
                                                                                                                                                                                                                                                                                                                                                                                      P39057;
                                                                                                                                                                                                                                                                                                                                                                                                              DYHC_ANTCR
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                                 MEDLINE=91326104; PubMed=1830928;
                                                            SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=7629;
                                                                                                                                                   Anthocidaris
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296 AA;
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(Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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34566 MW;
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24.2%;
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Last annotation update)
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                                                                                                                                                                              Echinacea; Echinoida;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN AQ_1923; 9C88F4456AA9449C CRC64;
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                01-AUG-1992
01-AUG-1992
15-JUN-2002
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 352:643-645(1991).
-I- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTU
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004273; Dynein_heavy. Pfam; PF03028; Dynein_heavy; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D01021; BAA00827.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Four ATP-binding sites in the midregion of the beta heavy chain
                                                               Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
Damagnez V.,
                                                      Schizosaccharomyces.
                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                    DNA polymerase alpha catalytic
                                                                                                                                                                 P28040;
                                                                                                                                                                           DPOA_SCHPO
        SEQUENCE FROM N.A. MEDLINE=91238692;
                                         NCBI_TaxID=4896
                                                                                                 POL1 OR SWI7 OR SPAC3H5.06C
                                                                                                                                                                                                                                  520 FKMLDCYGPLLDRPVIRNDF---ECKYPIVLMLYDQELDQSKEIYDEH 564
                                                                                                                                                                                                                                                                             460 EEFQECAKVFTERPYDGLDPTCQEFLEDYEEFEKKVFDLDRRLGSILCQGFDDCCGLEAA 519
                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                 1 EEREDCWTFYANRKY------TDFDKSFKKSSDLDE-----CK------KTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S17231; S17231.
                                                                                                                                                                                                                                                       FKTEYCY-----IVFEDTVNKECYYNVV---DGEELDQEKFVVDEN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil.
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1950
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22133
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 Tillit J.,
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161
          PubMed=2034212;
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 de Recondo A.-M., Baldacci G.;
                                                                                                                                                                                                                                                                                                                                                                                                                      MICROTUBULE-BINDING (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                        Score 74; DB 1
Pred. No. 81;
14; Mismatches
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ATP (POTENTIAL).
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                                                                             Schizosaccharomycetes;
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                     C465CC5C6C6D325D CRC64;
                                                                                                                                                                              1405
                                                                                                                                                                                                                                                                                                                                   DB 1; Length 4466; 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
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RA Collins M., Connor R., Lorent A., Harris D., Hidalgo J., Hodgson G., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J., RRA James K., Jones M., Leather S., McDonald S., McLean J., RRA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Moliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RRA Mcherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Squares S., Stevens K., RA Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., RRA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Bger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Gifeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S. M., Loas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G., Ra Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G., Ra Lucas M., Rochet M., Galilardin C., Tallada V.A., Forsburg S.L., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P., "The genome sequence of Schizosaccharomyces pombe.";
            TIGRFAMS; TIGR00592; pol2; 1.
PROSTTE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       Pfam; PF00136; DNA_pol_B; 1. Pfam; PF03104; DNA_pol_B_exo;
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X69673; CAB57881.1; -.
EMBL; Z99296; CAB16598.1; -.
PIR; S15993; DJZPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMASE IS A REPLICATIVE POLYMERASE.
-1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                            SMART; SM00486; POLBC;
                                                                                                                                                                                                                                                                                                                            InterPro; IPR002064; DNA_pol_B.
InterPro; IPR004578; Pol2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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                                                                                                                                                                                             PRINTS; PR00106; DNAPOLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93140876; PubMed=8423854; Jagmohan S., Klar A.J.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerases alpha."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULÁR LOCATION: Nuclear.
MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, GAMMA, DELTA, ALLERSTON WHICH ARE RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIFFERENT REACTIONS OF DNA SYNTHESIS.
SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboratic en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X58299; CAA41232.1;
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Nuclear protein
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P40157;
01-FEB-1995
P81034;
15-JUL-1998 (Rel. 36, Created)
                                                             MOH1_CANPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z71488; CAA96114.
SGD; S0005156; YNL212W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coster F., van Dyck L., Jonniaux J.-L., Purnelle B., Goffeau A.; "The sequence of a 13.5 kb DNA segment from the left arm of yeast chromosome XIV reveals MERI; RAPI; a new putative member of the DNA replication complex and a new putative serine/threonine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Hypothetical 88.8 kDa protein in PEXI7-MERI intergenic region.
YNL212W OR N1327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
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MEDLINE=95282517; PubMed=7762305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          řeast 11:85-91(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                       372
                                                                                                                                                                                                                                                                                                              315
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                      DCEGKDAGNAAGTGDESDEVDED
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Z71488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEDTVNKECYYNVVDGE-----ELDQEKFVVDEN---FTENYLTDCEGKDAGNAAGTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA96114.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAA55496.1;
                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO C.CARDUNCULUS PROTEIN CYPRO4 AND S.POMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88845 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          12.4%; Score 71;
26.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%;
32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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Pred. No.
                                                                                                                                                                                                                                                      103
                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCBB1F4CE32BF97C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P06596;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase A2 precursor (EC 3.1.1.4) (Phospholipase) (Group IB phospholipase A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth and reproduction.";
growth and reproduction.";
J. Biol. Chem. 271:12749-12754(1996).

J. Biol. Chem. 271:12749-12754(1996).

-I- FUNCTION: REPRESSES THE SYNTHESIS OF METHYL FARNESOATE, THE
PRECURSOR OF INSECT JUVENILE HORMONE III IN THE MANDIBULAR ORGAN.

-I- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN

-I- TISSUE SPECIFICITY: PRODUCED TO THE SINUS GLAND WHERE IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CANFA
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15-JUL-2002 (Rel. 41, Last annotation update)
Mandibular organ-inhibiting hormone-1 (MOIH-1).
Cancer pagurus (Rock crab).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Brachyura; Eubrachyura; Cancroidea; Cancridae; Cancer.
gene.
Eur.
[3]
                                                                        SEQUENCE FROM N.A.

MEDLINE-90306027; PubMed-2142076;

MEdfelec B., Laforge K.S., Vasiloudes

"Isolation and sequence of the canine
                                                                                                                                                                                                                             sequences
                                                                                                                                                                                                                                                                                Ohara O., Tamaki M., Na
Teraoka H., Okamoto M.;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-86223862;
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9615
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00550; HYPRGLYCEMIC. PROSITE; PS01250; CHH_MIH_GIH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01147; Crust_neurohorm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001166; CHH_MIH_GIH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Sinus gland;
MEDLINE-96278659; F
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SIMILARITY: BELONGS TO THE ARTHROPOD
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                                                                                                                                                                                                and rat pancreatic phospholipases A2: ences deduced from complementary DNAs. iochem. 99:733-739(1986).
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                          Biochem.
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                          190:299-304(1990)
                                                                                                                                                                                                                                                                                                     PubMed=3754861;
M., Nakamura E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TDFDKSFKKSSDLDECKKTCF-KTEY--CYIVFEDTVNKE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Carnivora; Fissipedia; Canidae;
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Pred. No. 2.5;
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8DB338A39058A62D CRC64;
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                                                                                                                                                                                                                                DNAS.";
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                                                                        P., Puigserver A., Scheele G.A., pancreatic phospholipase A2
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                                                                                                                                                                                                                                                                                                        Fujii Y., Shin
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EMBL; M35301; AAA3088;
PIR; A24392; PSDG.
PIR; S11316; S11316.
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-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
        ...eracting protein 1) (NIP1).
NCBP2 OR CBP20.
Homo car'
                                                                               P52298; Q14924;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
20 kDa nuclear cap binding protein (NCBP 20 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kerfelec B., Laforge K.S., Puigserver A., Scheel
"Primary structures of canine pancreatic lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pancreas 1:430-437(1986).
                                                                                                                                                                                                                             CB20_HUMAN
                                                                                                                                                                                                                                                              HUMAN
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SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
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   Q58285;
15-JUL-1998
15-JUL-1998
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Nuclear protein; RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN MEDIATING U SNRNA EXPORT FROM THE NUCLEUS BINDS TO 5'CAPPED MRNA.
-I- SUBUNIT: THE CAP-BINDING PROTEIN (CBC) COMPLEX IS AN HETERODIMEN OF CBP80 AND CBP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kataoka N., Ohno M., Moda I., Shimura Y.;
"Identification of the factors that interact with NCBP, an nuclear cap binding protein.";
Nucleic Acids Res. 23:3638-3641(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                          Ptam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
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Genew; HGNC:7659; NCBP2.
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McGuigan C., Mattaj A.W.;
"A cap-binding protein complex mediating U snRNA export.";
Nature 376:709-712(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                _METJA
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                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; pubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
                                                  Mol. Cell.
                                                                                                                      MEDLINE=96220458; PubMed=8649382; Luke M.M., della Seta F., di Como
                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome. SEQUENCE 748 AA; 90731 MW; 5515ED3B541562EA CRC64;
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            SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanocaldococcaceae; Methanocaldococcus
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                                            the SIT4 phosphatase.";
Cell. Biol. 16:2744-2755(1996).
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                                                                               a new family of proteins,
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Pred. No. 27;
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                                                                                                                    Sugimoto H., Kobayashi R.,
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"A 37.5 kb region of yeast chromosome X includes the SME1, MEFZ, GSH1 and CSD3 genes, a TCP-1-related gene, an open reading frame similar to the DAL80 gene, and a tRNA(Arg).";

Yeast 11:873-883(1995).

-1- FUNCTION: ASSOCIATES WITH THE SIT4 PHOSPHATASE IN A CELL CYCLE DEPENDENT MANURE. MAY BE DIRECTLY OR INDIRECTLY INVOLVED IN SIT4-DEPENDENT FUNCTIONS IN BUDDING AND IN NORMAL G1 CYCLIN
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EMBL; X85021; CAA59396.1; -.
EMBL; Z49373; CAA89392.1; -.
SGD; S0003634; SAP185.
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MEDLINE-96090136; PubMed-7483851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PTM: HYPERPHOSPHORYLATED IN THE ABSENCE OF SIT-4.
-!- SIMILARITY: BELONGS TO THE SAPS FAMILY.
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miosga T., Boles E., Schaaff-Gerstenschlaeger I., Schmitt S.,
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Result
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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573
1 EEREDCWTFYANRK
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Copyright (c) 1993 - 2003 Compugen Ltd.
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050667
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                                                          Q9k8n5 bacillus ha
097239 plasmodium
Q9vfh8 drosophila
Q8syg5 drosophila
Q8syg5 drosophila
Q03650 trypanosoma
Q20246 caenorhabdi
Q94648 plasmodium
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Q9x9s1 streptococc
Q9u2q4 caenorhabdi
Q9xts9 caenorhabdi
          Q9fiw8 arabidopsis
035821 rattus norv
Q9fk41 arabidopsis
050667 borrelia bu
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Q9nexO caenorhabdi		icobac		Q91kr9 arabidopsis	Q8sxs8 drosophila	Q94718 paramecium	Q22144 caenorhabdi	Q65239 african swi	Q.			Q9vir9 drosophila	٠.	9			Q9ha35 homo sapien	7		ø		Q9sks0 arabidopsis				9	Q9xv53 caenorhabdi	Q9v6s9 drosophila

ALIGNMENTS

RESULT 1 Q8XJ41

Q8XJ41

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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                          EMBL; AP003192; BAB81626.1;
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 3.
SMART; SM00028; TPR; 3.
                                                                                                                                                                                                                                                     Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anae: flesh-eater."; flesh-eater."; Flesh-eater."; Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                                          Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID-1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical CPE1920.
                                                                                                                                                                  Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=13 / TYPE A;
                                                                                                                                                                                                                                                                                                                                 PubMed=11792842;
36 FKTEYCYIVFEDTVNKECYYNV---VDGEELDQEKFV 69
                                            11
                                                                        10 YANRKYTDFDKSFKKSSDLDECK-----KTC 35
                                                                                                                      Local
                                         YNTRNYSDAINYYKKALDNDECKCHSYYNAGYCYIKLKQYEKAIEMITKALELYQDSKYF 70
                                                                                                                     Similarity
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116 AA; 13590 MW;
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein CPE1920.
                                                                                                                     13.7%; Score 78.5; DB 16; 22.7%; Pred. No. 1.9;
                                                                                                                                                             Complete proteome.
3590 MW; 9D6B5D847B3A7312 CRC64;
                                                                                                       11; Mismatches
                                                                                                       27;
                                                                                                                                   Length 116;
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Q9CQ49

Q9cq49

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71

FNLAYCYSMINNNSKALRYFNLAWALDNADIDCEKAI 107

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RESULT
Q9U2Q4
ID Q9
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DT Q9
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Best Local S
Matches 23
  Query Match
Best Local S
Matches 23
                                                                                      investigating biology.";
Science 282:2012-2018(1998).
EMBL; ALLIO478; CAB54340.1; -.
InterPro; IPR001304; Lectin_C.
SMART; SM00034; CLECT; 1.
SEQUENCE 550 AA; 62195 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9X9S1;
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"A single gene (tts) located outside the cap locus directs the formation of Streptococcus pneumoniae type 37 capsular polysaccharide: type 37 pneumococci are natural, genetically binary strains.";

J. Exp. Med. 19:241-251(1999).

EMBL; AJ131985; CAB51339.1; -.

InterPro; IPR001173; Glycos_transf_2.

Pfam; PF00535; Glycos_transf_2; 1.

SEQUENCE 509 AA; 58888 MW; C6C38DZACFABODBA CRC64;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae; Streptococcus.
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                                                                                                                                                                                                                                                               none
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                     'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 FETVILDDSKSEVY 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 TEYANRKYTDEDKSEKKSSDLDECKKTCFKTEYCYIVFEDTVN----KECYYNVVDGEELD
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23; Conserv
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       Conservative
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                                                                                                                                                                                                                                                                                  PubMed=9851916;
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                        13.7%;
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13,
17,
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    12;
  Score 78.5; D
Pred. No. 11;
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Best Local S
                                 UL-OCT-2000 (TREMBLrel. 15, Created)
01-OCT-2000 (TREMBLrel. 15, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Two-component sensor histidine kinase involved in chean OR BH2970.
BB24717---
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01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00022; EGF_1; UNKNOWN_8.
PROSITE; PS01186; EGF_2; 4.
EGF-like domain; Glycoprotein.
SEQUENCE 907 AA; 101840 MW; 88:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1078; AMINACHANNEL. PRINTS; PRO0010; EGFBLOOD. SMART; SM00181; EGF; 8.
Bacillus halodurans. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                     Q9K8N5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF000858; ASC; Pfam; PF00008; EGF;
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InterPro; IPR001438; EGF_II.
InterPro; IPR001873; Na+channe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z98877; CAB11570.1;
HSSP; Q12784; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McMurray A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                             226
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                                                                                                                                                                                                                                                                                                   280 VNSRCI--VYEAGEME-----TDPNACEDNSTLC-GAELGHGMCINWQSDVTD
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                                                                                                                                                                                                                                                                                                                                                                                                                     10 YANRKYTDFDKSFK------KSSDL------DECKKTC--FKTEYCYIVFEDT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
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                                                                                                                                                                                                                                                                                                                                             VNKECYYNVVDGEELDQEKFVVDENFTENYLTDCEGKDAGNAAGTGDESDEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYYDKDSKECWWWSIDNVHF-LEKVHPSEN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFEDTVNKECYYNVVDGEELDQEKFVVDEN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGNFLHNRPYPDSCETECMDTMVQVNAKPGPLMGSRNIKDNLTSSDECVKYCWKDLNCFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
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                                                                                                                                                                                     PRELIMINARY;
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29.2%;
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  Bacillus/Clostridium
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12,
20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8B55FF139F8F81D7 CRC64;
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                                                                                                                                                                                       682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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  group;
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                                                                     in chemotaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 907;
    Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Bacillaceae; Bacillus

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                                                                                                                                                                                                                                                                                             097239
                     MEDLINE-99376085; PubMed=10448855;
Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M, Devlin K., Feltwell T.,
Chentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Horns
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quali M.A., Rajandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
"The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last segi
01-DEC-2001 (TrEMBLrel. 19, Last anni
Hypothetical 467, 9 kDa protein.
PEC0245C, MAL3P2.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Si
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00387; HATPase_c; 1.
SMART; SM00073; HPT; 1.
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Nature 400:532-538(1999).
                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=86665;
           falciparum .
                                                                                                                                                                                      NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                              213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PF02895; H-kina
; PF02518; HATPaa;
; PF01627; Hpt;
                                                                                                                                                                                                                                                                                                                                                                                                      EELDQEKFVVDENFTENYLTDCEGKD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                 YDEFEMTVLDQSFEQGYQAYQIEVTLDE--KTLLKAARVFMVFEVLEQVG-EVIKSTPSA 212
                                                                                                                                                                                                                                                                                                                                                                             EELEEEKF -- DERFLYTLITKVDGEE 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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IPR004105; H-kinase_dim.
IPR004359; HIS_KIN_sig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002570;
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IPR004358; Bact_sens_pr_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682 AA;
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic sequence comparison with Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75272 MW;
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32.6%;
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                                                                                                                                                                                                                                                       Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                 Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                             3933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Sasaki R., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
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  RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D., Celniker S.E., Lih P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harris H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchar A.,
RA Horriy J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gduan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravita S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravita S., Kulp D., Lai Z.,
RA Melkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hostin D., Holland G.S., Pan S., Warp D. M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wellston G.S., Banker S., Wenter E., Wang A.H., Wang X.,
Ran G., Wang S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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01-MAY-2000
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PROSITE; PS00018; EF_HAND; UNKNOWN_1.
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01-JUN-2001
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(TremBLrel. 13, Last seq
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Myers E.W., Rubin G.M., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
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CG14853.
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                                        Eukaryota; Euglenozoa;
NCBI_TaxID=5702;
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Stapleton "
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         SEQUENCE FROM N.A
                                                                                Trypanosoma brucei brucei
                                                                                                                    Cysteine-rich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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ch, acidic integral membrane protein p
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MEDLINE=90355963; PubMed=1697030;
Lee G.S.M., Bihain B.E., Russell D.G., Deckelbaum R.J., Ploeg L.H.;
"Characterization of a cDNA encoding a cysteine-rich cell surface
protein located in the flagellar pocket of the protozoan Trypanosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: SUPPOSED TO FUNCTION AS CELL SUI
INVOLVED IN RECEPTOR-MEDIATED ENDOCYTOSIS
-i- SUBCELLULAR LOCATION: CELL SURFACE; CONCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO EUKARYOTIC CELL SURFACE RECEPTORS, ESPECIALLY TO THE HUMAN LOW-DENSITY LIPOPROTEIN (LDL) RECEPTOR (P01130).
CAUTION: CONCERNING THE CONSENSUS SEQUENCE DDCN/DITGDCNET OF THE DODECAPEPTIDE REPEATS: UP FROM AA 316 IT IS UNSURE IF IT IS AMI
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                                                         N-LINKED
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Plasmodium

associated with

Bonnefoy S.,

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RESULT 10
Q20246
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Best Local
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                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; 277661; CAB01183.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae;
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                                        CYYNVVDGEELDQEKF-VVDENFTE--NYLTDCEGKDAGNAAGTGDESDEVD
                                                                                                       EEREDCWTFYANRKYTDFDKSFKK-SSDLDECKKTCFKTEYCYIVFE-----DTVNKE 52
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                                                                       EESEDC-----FEKVFLAIISGKHECSK-----DYDFLARNLIQRREALTSGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEREDCWTFYANRKYTDFDKSFKKSSD-LDECKKT--CFKTEYCYIVFEDTVNKECYYNV 57
                                                                                                                                                                                                                          PF03236;
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                                                                                                                                                                                                                                                                                                                                                                                    (JUL-1996)
                                                                                                                                                                                                         264 AA;
                                                                                                                                          Conservative
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                           <u>:</u>
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28.0%;
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                                                                                                                                          19;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                       FD237BB5704362C4 CRC64;
                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    databases
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Best Local
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Q94648;
01-FEB-1997
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2002 (TrEMBLrel. 20,
6)[AAF22924.1 (Hypothetical
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SEQUENCE
                                                                                    "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,013,767
physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                Q9FIW8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1786 K-KKNKKNVENQEKEFYVLNKIFVHNFI 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barale J.C., Candelle D., Attal-Bonnefoy G., Dehoux P., Bonnefoy S. Ridley R., Pereira da Silva L., Langsley G.; Pereira da Silva L., Langsley G.; Plasmodium falciparum AARP1, a giant protein containing repeated motifs rich in asparagine and aspartate residues, is associated with motifs and saparagine and aspartate residues.
                       Lee
                                                                                                                                                                                                                                                                                                                                     AT5G39780
                                                                                                                                                                                                                                                                                                                                                                                                                                Q9FIW8
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                                                                                                                                                                                                       STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001841; Znf_ring.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the infected erythrocyte membrane."; Infect. Immun. 65:3003-3010(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum
                                                    SEQUENCE
                                                                                                                                                                      Nakamura
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=36329;
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                                   ľamada K.,
                                                                                                                                                      Cabata S
                                                                                                                                                                                 MEDLINE=99087489;
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                      J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDSEECQIKESYKKMSECNNKENIIFDSISVLRKNNIKRLKNYMCKNKNCYIYYDDNNNK 1785
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. FROM N.A.
(., Banh J., Chang C.H., Cha.
Onodera C.S., Quach H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                  Y., Sato
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3844
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                                                                                                                                                                  PubMed=9872454;
S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3844
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23.9%;
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Best Local
Q9FK41;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                     Comte P.A., Ossipow V., Schibler U.; "Isolation of PIP, a 160 kDa nucleolar protein that interacts activation domain of PAR transcription factors."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. EMBL; U83590; AAB62878.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cl Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumanr Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                Wuarin J., Schibler U.; "Expression of the liver-enriched transcriptional activator protein DBP follows a stringent circadian rhythm."; Cell 63:1257-1266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 01-JAN-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
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                                       Q9FK41
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MEDLINE=91084854; PubMed=2261643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            035821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAR interacting protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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                                                                                                                          GEELDQE--KFVVDENFTENYLTDCEGKDAGNAAGTGDESDE
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                                                                                                         GEESEEEDRDKDVDPGFRQQLM---EVLQAGNALGGEEEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length cDNA of gene At5g39780 (GI:15242471).";
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27.7%; Pr
tive 19;
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Pred. No. 29;
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                                       PRT;
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sequence update)
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Kamiya A., Karlin-Neumann
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01-JUN-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwin Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.
                                                                                       PRINTS; PR00507; N12N6MTFRASE.
PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     050667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones."; DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                SEQUENCE
                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid lp28-3.
Bacteria; Spirochaetales;
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                                                                                                                                             InterPro; IPR002296;
InterPro; IPR002052;
                                                                                                                                                                                                                                                 Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                      burgdorferi
                                                                                                                                                                                                                                                                                                                      Smith H.O., Venter J.C.;
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                                                                                                                                                                                                                                                                                        "Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001798; Kelch.
Pfam; PF01344; Kelch; 6.
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                                                                                                                                                                                                                                                                                                                                           Roberts K., Hatch B.,
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Length 1278;
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